AMENDMENTS TO THE SPECIFICATION

Please replace the Examples section beginning on page 371, line 5 of the substitute specification, with the following amended Examples section:

-- **Examples**

Description of the Preferred Embodiments

Example 1 – Method Of Identifying The Novel BMY_HPP Human Phosphatases Of The Present Invention.

Polynucleotide sequences encoding the novel BMY_HPP phosphoprotein phosphatases of the present invention were identified by a combination of the following methods:

Homology-based searches using the TBLASTN program [Altschul, 1997] to compare known phosphoprotein phosphatases with human genomic (gDNA) and EST sequences. EST or gDNA sequences having significant homology to one or more of the known phosphatases listed in Table III (expect score less than or equal to $1x10^{-3}$) were retained for further analysis.

Hidden Markov Model (HMM) searches using PFAM motifs (listed in Table IV) [Bateman, 2000 #9; Sonnhammer, 1997] were used to search human genomic sequence using the Genewise program. EST or gDNA sequences having a significant score (greater than or equal to 10) with any of the following motifs were retained for further analysis.

HMM searches using PFAM motifs (listed in Table IV) were used to search predicted protein sequences identified by GENSCAN analysis of human genomic sequence [Burge, 1997 #10]. gDNA sequences having a significant score (greater than or equal to 10) with any of the following motifs were retained for further analysis.

Table IV: PFAM motifs used to identify phosphoprotein phosphatases

Motif Name	PFAM Accession No.	Description
DSPc	PF00782	Dual specificity phosphatase, catalytic domain
ST_phosphatase	PF00149	Ser/Thr protein phosphatase
Y_phosphatase	PF00102	Protein-tyrosine phosphatase

Once a bacterial artificial chromosomes (Backs) encoding a novel phosphoprotein phosphatase was identified by any one of the methods above, additional potential axons were

identified using GENSCAN analysis of all nearby Backs (identified by the Golden Path tiling map, UCSC). Intron/exon boundaries, transcript cDNA sequence and protein sequence were determined using GENSCAN. The predicted protein sequence were used to identify the most closely related known phosphatase using the BLASTP program as described in herein.

In the case of BMY_HPP5, BMY_HPP5 was identified as an Incyte EST (ID 4155374) with homology to known protein phosphatases and significant expression in the central nervous system. The Incyte clone sequence was used to design oligonucleotides for isolation of additional cDNAs. Such cDNAs have been recovered and sequenced and compared to a full-length Incyte template (assembly of EST sequences) (ID1026659.7). The BMY_HPP5 cDNA has significant identity to Incyte 1026659.7 but diverges at the five-prime and three-prime ends, suggesting that it may be an alternatively spliced product of the same gene.

Example 2 - Cloning of the Novel Human BMY_HPP Phosphatases Of The Present Invention.

A variety of methods known in the art may be used for cloning the novel BMY_HPP phosphatases of the present invention. Briefly, using the predicted or observed cDNA sequences for the BMY-HPP genes of the present invention, antisense oligonucleotides with biotin on the 5' end could be designed (the sequences of these oligos are provided in Table VI). These oligos will be used to isolate cDNA clones according to the following procedure:

One microliter (one hundred and fifty nanograms) of a biotinylated oligo is added to six microliters (six micrograms) of a mixture of single-stranded covalently closed circular cDNA libraries (such libraries are commercially available from Life Technologies, Rockville, Maryland, or may be created using routine methods known in the art) and seven microliters of 100% formamide in a 0.5 ml PCR tube. The cDNA libraries used for specific BMY_HPP genes will be determined by the results of the expression patterns as described herein.

The mixture is heated in a thermal cycler to 95° C for 2 mins.

Fourteen microliters of 2X hybridization buffer (50% formamide, 1.5 M NaCl, 0.04 M $NaPO_4$, pH 7.2, 5 mM EDTA, 0.2% SDS) wis added to the heated probe/cDNA library mixture and incubated at 42° C for 26 hours.

Hybrids between the biotinylated oligo and the circular cDNA are isolated by diluting the hybridization mixture to 220 microliters in a solution containing 1 M NaCl, 10 mM Tris-HCl pH 7.5,

1mM EDTA, pH 8.0 and adding 125 microliters of streptavidin magnetic beads. This solution is incubated at 42° C for 60 mins, mixing every 5 mins to resuspend the beads.

The beads are separated from the solution with a magnet and the beads washed three times in 200 microliters of 0.1 X SSPE, 0.1% SDS at 45° C.

The single stranded cDNAs are released from the biotinlyated oligo/streptavidin magnetic bead complex by adding 50 microliters of 0.1 N NaOH and incubating at room temperature for 10 mins.

The cDNAs are precipitated by adding six microliters of 3 M Sodium Acetate , 5 micrograms of glycogen and 120 microliters of 100% ethanol followed by centrifugation.

The cDNAs are resuspended in 12 microliters of TE (10 mM Tris-HCl, pH 8.0), 1mM EDTA, pH 8.0).

The single stranded cDNAs are converted into double stranded molecules in a thermal cycler by mixing 5 microliters of the captured DNA with 1.5 microliters of a standard SP6 primer (homologous to a sequence on the cDNA cloning vector) at 10 micromolar concentration and 1.5 microliters of 10 X PCR buffer. The mixture is heated to 95° C for 20 seconds, then ramped down to 59 ° C. At this time 15 microliters of a repair mix preheated to 70° C is added (repair mix contains 4 microliters of 5 mM dNTPs (1.25 mM each), 1.5 microliters of 10X PCR buffer, 9.25 microliters of water, and 0.25 microliters of Taq polymerase). The solution is ramped back to 73° C and incubated for 23 mins.

The repaired DNA was precipitated as described above and resuspended in 10 microliters of TE.

Two microliters of double-stranded cDNA are used to transform E. coli DH12S cells by electroporation.

The resulting colonies are screened by PCR, using a primer pair designed to identify the proper cDNAs (primer sequences, as provided in Table VI, may be used).

Those cDNA clones that are positive by PCR are then assessed to determine the inserts size. Two clones for each BMY_HPP gene are chosen for DNA sequencing using standard methods known in the art and described herein.

The polynucleotide(s) of the present invention, the polynucleotide encoding the polypeptide of the present invention, or the polypeptide encoded by the deposited clone may represent partial, or incomplete versions of the complete coding region (i.e., full-length gene). Several methods are

known in the art for the identification of the 5′ or 3′ non-coding and/or coding portions of a gene which may not be present in the deposited clone. The methods that follow are exemplary and should not be construed as limiting the scope of the invention. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5′ and 3′ "RACE" protocols that are well known in the art. For instance, a method similar to 5′ RACE is available for generating the missing 5′ end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993)).

Briefly, a specific RNA oligonucleotide is ligated to the 5′ ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5′ portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full-length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5′ phosphate groups on degraded or damaged RNA that may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5′ ends of messenger RNAs. This reaction leaves a 5′ phosphate group at the 5′ end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5′ end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5′ end sequence belongs to the desired gene. Moreover, it may be advantageous to optimize the RACE protocol to increase the probability of isolating additional 5' or 3' coding or non-coding sequences. Various methods of optimizing a RACE protocol are known in the art, though a detailed description summarizing these methods can be found in B.C. Schaefer, Anal. Biochem., 227:255-273, (1995).

An alternative method for carrying out 5' or 3' RACE for the identification of coding or non-coding sequences is provided by Frohman, M.A., et al., Proc.Nat'l.Acad.Sci.USA, 85:8998-9002 (1988). Briefly, a cDNA clone missing either the 5' or 3' end can be reconstructed to include the

absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start of translation. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNAs reverse transcribed with Superscript II (Gibco/BRL) and an antisense or I complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoIJ SaiI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., Nucleic Acids Res., 19:5227-32(1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a

symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3'RACE. While the full-length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5'RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., Nucleic Acids Res., 21(7): 1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably 30 containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant family.

Representative primers for cloning any one of the human phosphatases of the present invention are provided in Table VI herein as 'Left Cloning Primer', 'Right Cloning Primer',

'Internal RevComp Cloning Primer', and/or 'Internal Cloning Primer'. Other primers could be substituted for any of the above as would be appreciated by one skilled in the art.

In the case of the full-length BMY_HPP1, BMY_HPP1 was cloned using the polynucleotide sequences of the identified BMY_HPP1 fragments BMY_HPP1_A (SEQ ID NO:1) and BMY_HPP1_B (SEQ ID NO:3) to design the following antisense 80 bp oligo with biotin on the 5' end:

Name	Sequence
Phos4-80b	5'bTGACAATGGATAGCTACTTTTCCTTCCTGTAAGGCAAATGTCATC ACCTTCACCATATCTAGGATAGTAGTAAGAGACGC -3 (SEQ ID NO:45)

One microliter (one hundred and fifty nanograms) of the gel-purified biotinylated PCR fragment was added to six microliters (six micrograms) of a single-stranded covalently closed circular brain, fetal brain, bone marrow, prostate, spleen, testis, and thymus cDNA libraries and seven microliters of 100% formamide in a 0.5 ml PCR tube. The mixture was heated in a thermal cycler to 95° C for 2 mins. Fourteen microliters of 2X hybridization buffer (50% formamide, 1.5 M NaCl, 0.04 M $NaPO_4$, pH 7.2, 5 mM EDTA, 0.2% SDS) was added to the heated probe/cDNA library mixture and incubated at 42° C for 26 hours. Hybrids between the biotinylated oligo and the circular cDNA were isolated by diluting the hybridization mixture to 220 microliters in a solution containing 1 M NaCl, 10 mM Tris-HCl pH 7.5, 1mM EDTA, pH 8.0 and adding 125 microliters of streptavidin magnetic beads. This solution was incubated at 42° C for 60 mins, mixing every 5 mins to resuspend the beads. The beads were separated from the solution with a magnet and the beads washed three times in 200 microliters of 0.1 X SSPE, 0.1% SDS at 45° C.

The single stranded cDNAs were released from the biotinlyated probe/streptavidin magnetic bead complex by adding 50 microliters of 0.1 N NaOH and incubating at room temperature for 10 mins. Six microliters of 3 M Sodium Acetate was added along with 15 micrograms of glycogen and the solution ethanol precipitated with 120 microliters of 100% ethanol. The DNA was resuspend in 12 microliters of TE (10 mM Tris-HCl, pH 8.0), 1mM EDTA, pH 8.0). The single stranded cDNA was converted into double strands in a thermal cycler by mixing 5 microliters of the captured DNA with 1.5 microliters 10 micromolar standard SP6 primer (homologous to a sequence on the cDNA cloning vector) and 1.5 microliters of 10 X PCR buffer. The mixture was heated to 95° C for 20

seconds, then ramped down to 59 ° C. At this time 15 microliters of a repair mix, that was preheated to 70° C (Repair mix contains 4 microliters of 5 mM dNTPs (1.25 mM each), 1.5 microliters of 10X PCR buffer, 9.25 microliters of water, and 0.25 microliters of Taq polymerase). The solution was ramped back to 73° C and incubated for 23 mins. The repaired DNA was ethanol precipitated and resuspended in 10 microliters of TE. Two microliters were electroporated in E. coli DH12S cells and resulting colonies were screened by PCR, using the following primer pair number:

Name	Sequence
Phos2-2s	TACAATTTCGGATGGAAGGATTAT (SEQ ID NO:154)
Phos2-2a	GCATGACAATGGATAGCTACTTT (SEQ ID NO:155)

The sequence of the BMY_HPP1 polynucleotide was sequenced and is provided in Figures 20A-D (SEQ ID NO:149).

In the case of the full-length BMY_HPP2, BMY_HPP1 was cloned using the polynucleotide sequences of the identified BMY_HPP2 fragment (SEQ ID NO:5) to design the following antisense 80 bp oligo with biotin on the 5' end:

Name	Sequence
Phos2-80b	5'bGTGCCGCACGCCCAGGTCCAACAGGAACTGGTAGTGGGCGGGG AGCCGCGGCAGCGCCAGTCCCGCCAGCCGGCCCGGA -3 (SEQ ID NO:51)

One microliter (one hundred and fifty nanograms) of the gel-purified biotinylated PCR fragment was added to six microliters (six micrograms) of a single-stranded covalently closed circular brain, fetal brain, bone marrow, prostate, spleen, testis, and thymus cDNA libraries and seven microliters of 100% formamide in a 0.5 ml PCR tube. The mixture was heated in a thermal cycler to 95° C for 2 mins. Fourteen microliters of 2X hybridization buffer (50% formamide, 1.5 M NaCl, 0.04 M $NaPO_4$, pH 7.2, 5 mM EDTA, 0.2% SDS) was added to the heated probe/cDNA library mixture and incubated at 42° C for 26 hours. Hybrids between the biotinylated oligo and the circular cDNA were isolated by diluting the hybridization mixture to 220 microliters in a solution containing 1 M NaCl, 10 mM Tris-HCl pH 7.5, 1mM EDTA, pH 8.0 and adding 125 microliters of streptavidin magnetic beads. This solution was incubated at 42° C for 60 mins, mixing every 5 mins

to resuspend the beads. The beads were separated from the solution with a magnet and the beads washed three times in 200 microliters of 0.1 X SSPE, 0.1% SDS at 45° C.

The single stranded cDNAs were released from the biotinlyated probe/streptavidin magnetic bead complex by adding 50 microliters of 0.1 N NaOH and incubating at room temperature for 10 mins. Six microliters of 3 M Sodium Acetate was added along with 15 micrograms of glycogen and the solution ethanol precipitated with 120 microliters of 100% ethanol. The DNA was resuspend in 12 microliters of TE (10 mM Tris-HCl, pH 8.0), 1mM EDTA, pH 8.0). The single stranded cDNA was converted into double strands in a thermal cycler by mixing 5 microliters of the captured DNA with 1.5 microliters 10 micromolar standard SP6 primer (homologous to a sequence on the cDNA cloning vector) and 1.5 microliters of 10 X PCR buffer. The mixture was heated to 95° C for 20 seconds, then ramped down to 59 ° C. At this time 15 microliters of a repair mix, that was preheated to 70° C (Repair mix contains 4 microliters of 5 mM dNTPs (1.25 mM each), 1.5 microliters of 10X PCR buffer, 9.25 microliters of water, and 0.25 microliters of Taq polymerase). The solution was ramped back to 73° C and incubated for 23 mins. The repaired DNA was ethanol precipitated and resuspended in 10 microliters of TE. Two microliters were electroporated in E. coli DH12S cells and resulting colonies were screened by PCR, using the following primer pair number:

Name	Sequence
Phos2-2s	GAGAAAGCAGTCTTCCAGTTCTAC (SEQ ID NO:156)
Phos2-2a	ATGGGAGCTAGAGGGTTTAATACT (SEQ ID NO:157)

The sequence of the BMY_HPP2 polynucleotide was sequenced and is provided in Figure 21 (SEQ ID NO:151).

In the case of BMY_HPP5, BMY_HPP5 was cloned using the sequence of Incyte clone 4155374 to design the following PCR oligos:

Oligo number	Name	Sequence
686	4155374-C3.s	5'-GGCCAAAGAGCAAACTCAAG-3 (SEQ ID NO:69)
687	4155374-C3.Ba	5'-bGCATAGCTTGTTGGTCCCAT-3 (SEQ ID NO:70)

A biotinylated nucleotide was included on the 5' end of oligo 687. Using the PCR primer pair, a 414bp biotinylated fragment was amplified using the Incyte clone as the template. The fragment was gel purified by agarose electrophoresis and stored at 4° C. The same PCR primer pair

was used to screen cDNA libraries for the presence of homologous sequences. Positive PCR results were obtained in our HPLC-size fractionated brain and testis libraries. One microliter (one hundred and fifty nanograms) of the gel-purified biotinylated PCR fragment was added to six microliters (six micrograms) of a single-stranded covalently closed circular testis cDNA library and seven microliters of 100% formamide in a 0.5 ml PCR tube. The mixture was heated in a thermal cycler to 95° C for 2 mins. Fourteen microliters of 2X hybridization buffer (50% formamide, 1.5 M NaCl, 0.04 M $NaPO_4$, pH 7.2, 5 mM EDTA, 0.2% SDS) was added to the heated probe/cDNA library mixture and incubated at 42° C for 26 hours. Hybrids between the biotinylated oligo and the circular cDNA were isolated by diluting the hybridization mixture to 220 microliters in a solution containing 1 M NaCl, 10 mM Tris-HCl pH 7.5, 1mM EDTA, pH 8.0 and adding 125 microliters of streptavidin magnetic beads. This solution was incubated at 42° C for 60 mins, mixing every 5 mins to resuspend the beads. The beads were separated from the solution with a magnet and the beads washed three times in 200 microliters of 0.1 X SSPE, 0.1% SDS at 45° C.

The single stranded cDNAs were released from the biotinlyated probe/streptavidin magnetic bead complex by adding 50 microliters of 0.1 N NaOH and incubating at room temperature for 10 mins. Six microliters of 3 M Sodium Acetate was added along with 15 micrograms of glycogen and the solution ethanol precipitated with 120 microliters of 100% ethanol. The DNA was resuspend in 12 microliters of TE (10 mM Tris-HCl, pH 8.0), 1mM EDTA, pH 8.0). The single stranded cDNA was converted into double strands in a thermal cycler by mixing 5 microliters of the captured DNA with 1.5 microliters 10 micromolar standard SP6 primer (homologous to a sequence on the cDNA cloning vector) and 1.5 microliters of 10 X PCR buffer. The mixture was heated to 95° C for 20 seconds, then ramped down to 59 ° C. At this time 15 microliters of a repair mix, that was preheated to 70° C (Repair mix contains 4 microliters of 5 mM dNTPs (1.25 mM each), 1.5 microliters of 10X PCR buffer, 9.25 microliters of water, and 0.25 microliters of Taq polymerase). The solution was ramped back to 73° C and incubated for 23 mins. The repaired DNA was ethanol precipitated and resuspended in 10 microliters of TE. Two microliters were electroporated in E. coli DH12S cells and resulting colonies were screened by PCR, using the primer pair number 686/687. The sequence of the BMY_HPP5 polynucleotide was sequenced and is provided in Figures 5A-E (SEQ ID NO:41).

Example 3 – Expression Profiling Of The Novel Human BMY_HPP Phosphatase Polypeptides Of The Present Invention.

PCR primers designed from the predicted or observed cDNA sequences (described elsewhere herein) will be used in a real-time PCR assay to determine relative steady state mRNA expression levels of BMY_HPP1, BMY_HPP2, BMY_HPP3, and BMY_HPP4 across a panel of human tissues according to the following protocol.

First strand cDNA may be synthesized from commercially available mRNA (Clontech) and subjected to real time quantitative PCR using a PE 5700 instrument (Applied Biosystems, Foster City, CA) using the manufacturers recommended protocol. This instrument detects the amount of DNA amplified during each cycle by the fluorescent output of SYBR green, a DNA binding dye specific for double strands. The specificity of the primer pair for its target may be verified by performing a thermal denaturation profile at the end of the run which provides an indication of the number of different DNA sequences present by determining melting Tm. Only primer pairs giving a single PCR product are considered. Contributions of contaminating genomic DNA to the assessment of tissue abundance may be controlled by performing the PCR with first strand made with and without reverse transcriptase. Only samples where the contribution of material amplified in the no reverse transcriptase controls was negligible are considered.

Small variations in the amount of cDNA used in each tube can be determined by performing a parallel experiment using a primer pair for the cyclophilin gene, which is expressed in equal amounts in all tissues. The data is then used to normalize the data obtained with each primer pair. The PCR data was converted into a relative assessment of the difference in transcript abundance amongst the tissues tested.

Representative primers for expression profiling analysis for each gene are provided in Table VI herein as 'EP Sense' and 'EP Anti-sense Primer', though may also include one or more of the following: 'Left Cloning Primer', 'Right Cloning Primer', 'Internal RevComp Cloning Primer', and/or 'Internal Cloning Primer'. Other primers could be substituted for any of the above as would be appreciated by one skilled in the art.

In the case of BMY_HPP1, the following PCR primer pair was used to measure the steady state levels of BMY_HPP1 mRNA by quantitative PCR:

Sense: 5'- TACAATTTCGGATGGAAGGATTAT -3' (SEQ ID NO:154)
Antisense: 5'- GCATGACAATGGATAGCTACTTT -3' (SEQ ID NO:155)

Briefly, first strand cDNA was made from commercially available mRNA. The relative amount of cDNA used in each assay was determined by performing a parallel experiment using a primer pair for a gene expressed in equal amounts in all tissues, cyclophilin. The cyclophilin primer pair detected small variations in the amount of cDNA in each sample and these data were used for normalization of the data obtained with the primer pair for the novel BMY_HPP1. The PCR data was converted into a relative assessment of the difference in transcript abundance amongst the tissues tested and the data is presented in Figure 22. Transcripts corresponding to BMY_HPP1 were expressed highly in testis; to a significant extent, in the spinal cord, and to a lesser extent, in pancreas, brain, pituitary, heart, and lung.

In the case of BMY_HPP2, the following PCR primer pair was used to measure the steady state levels of BMY_HPP2 mRNA by quantitative PCR:

Sense: 5'- GAGAAAGCAGTCTTCCAGTTCTAC -3' (SEQ ID NO:156)
Antisense: 5'- ATGGGAGCTAGAGGGTTTAATACT -3' (SEQ ID NO:157)

Briefly, first strand cDNA was made from commercially available mRNA. The relative amount of cDNA used in each assay was determined by performing a parallel experiment using a primer pair for a gene expressed in equal amounts in all tissues, cyclophilin. The cyclophilin primer pair detected small variations in the amount of cDNA in each sample and these data were used for normalization of the data obtained with the primer pair for the novel BMY_HPP2. The PCR data was converted into a relative assessment of the difference in transcript abundance amongst the tissues tested and the data is presented in Figure 23. Transcripts corresponding to BMY_HPP2 were expressed highly in liver and kidney; to a significant extent, in the spleen, and to a lesser extent, in lung, testis, heart, intestine, pancreas, lymph node, spinal cord, and prostate.

In the case of BMY_HPP5, the following PCR primer pair was used to measure the steady state levels of BMY_HPP5 mRNA by quantitative PCR:

Sense: 5'- ATGGGACCAACAAGCTATGC -3' (SEQ ID NO:67)
Antisense: 5'- TTATCAGGACTGGTTTCGGG -3' (SEQ ID NO:68)

Briefly, first strand cDNA was made from commercially available mRNA. The relative amount of cDNA used in each assay was determined by performing a parallel experiment using a primer pair for a gene expressed in equal amounts in all tissues, cyclophilin. The cyclophilin primer pair detected small variations in the amount of cDNA in each sample and these data were used for normalization of the data obtained with the primer pair for the novel BMY_HPP5. The PCR data was converted into a relative assessment of the difference in transcript abundance amongst the tissues tested and the data is presented in Figure 11. Transcripts corresponding to BMY_HPP5 were expressed highly in the testis, spinal cord, an to a lesser extent in bone marrow, brain, thymus, and liver.

Example 4 – Method of Assaying The Phosphatase Activity of the BMY_HPP Polypeptides of the present invention.

The Phosphatase Activity of the BMY_HPP Polypeptides of the present invention may be assessed through the application of various biochemical assays known in the art and described herein.

Hydrolysis of para-nitrophenyl phosphate

The phosphatase activity for BMY_HPP proteins may be measured by assaying the ability of the proteins to hydrolyze para-nitrophenyl phosphate, a compound known to be a substrate for phosphatases, as described in Krejsa, C. et al., J. Biol. Chem. Vol. 272, p.11541-11549, 1997 (which is hereby incorporated in its entirety herein). The proteins are incubated in 3 mg/ml para-nitrophenyl phosphate in a solution containing 60 mM MES, pH 6.0, 5% glycerol, 5 mM dithiothreitol, and 0.1% Triton X-100 for 15 min, or such other time as may be desired. The pH of the reaction may be varied to provide an optimal pH for each individual BMY_HPP protein by those with ordinary skill in the art of enzyme assays. The phosphatase reaction is stopped by the addition of 3 N NaOH to give a final NaOH concentration of 0.7 M. The product of the reaction is measured by reading the absorbance of the solution at 405 nm.

Two dimensional gel electrophoresis

The BMY_HPP polynucleotides of the present invention may be subcloned into appropriate vectors for expression in host cells. Representative vectors are known in the art and described herein.

2-D gel electrophoresis (IEF followed by SDS-PAGE) will be used to assay BMY_HPP-dependent dephosphorylation of host cell proteins. These proteins can be recovered from the gel and identified by mass spectrometric or other protein sequencing techniques known in the art.

Briefly, Methods for 2-dimensional gel analysis and labeling cells with proteins are well known in the art. Cells would be labeled with 32P orthophosphate, cellular proteins would be resolved on 2D gels and their positions determined by autoradiography. Proteins of interest would be identified by excising the spots and analyzing their sequence by mass spectroscopy. The following paper and the references therein describe the methods of labeling cells, analyzing the proteins on 2D gels and mass spec identification: Gerner, C. et al., J. Biol. Chem., Vol. 275, p.39018 - 39026, 2000. Substrates affected by the phosphatase would be identified by comparing wild type cells to cells where expression of the phosphatase is inhibited by deletion, anti-sense, or other means. Proteins whose phosphorylation increased would be either direct substrates or indirectly regulated by the phosphatase. Conversely, in cells where the active phosphatase was overexpressed, proteins whose phosphorylation decreased would either be direct substrates or indirectly regulated by the phosphatase.

Example 5 – Method of Identifying The Substrate of the BMY_HPP Phosphatase Polypeptides of the present invention.

Substrate identification

Protein substrates for BMY_HPP polypeptides of the present invention may be identified by recovery of proteins dephosphorylated in the 2-D gel electrophoresis assay described above. Phosphopeptide substrates may also be identified as proteins whose phosphorylation increases when the activity or expression of a BMY_HPP protein is decreased (for example, by an antibody, antisense or double-stranded inhibitory RNA or by a small molecule inhibitor of BMY_HPP activity). In either case, mass spectrometry can be used to identify the recovered proteins.

Phosphopeptide substrates for BMY-HPP polypeptides may also be identified by incubation of a phosphopeptide library with a catalytically inactive version of the protein, recovery of the complex, and peptide sequencing by standard methods such as Edman degradation or mass spectrometry.

Phosphopeptide substrates can also be identified by expressing a substrate trapping mutant phosphatase (one that is catalytically inactive due to active site mutation) and isolating the proteins that bind preferentially to the substrate trapping phosphatase relative to the wild type phosphatase.

Example 6 – Method of Identifying RET31 of the Present Invention.

In an effort to identify gene products involved in regulatory events, the RNA expressed in TNF-α-stimulated human lung microvascular endothelial cells was analyzed. Resting cells were stimulated for 1 h with TNF-α, and the RNA was isolated from the cells. Complementary DNA (cDNA) was created from the isolated RNA using methods known in the art. The cDNA that were upregulated in response to TNFα were identified using subtractive hybridization. A clone corresponding to a portion of the RET31 polynucleotide was identified and used to identify the full-length (SEQ ID NO:115). Additional methods are provided below.

HMVEC Cell culture

Primary cultures of human lung microvascular endothelial cells (HMVEC), from a single donor, were obtained from Clonetics (Walkersville, MD). The cells were grown in the endothelial cell growth medium-2 kit (CC-3202) with 5% Fetal Bovine Serum (Hyclone). Initially, the cells were seeded into a T-25 flask and, after reaching approximately 90% confluence, they were trypsinized and transferred into T-225 flasks at 1.2 x 10^6/flask in 80 mls of medium. For normal growth conditions, the medium was changed each 48 h. When the cells reached approximately 90% confluence, they were passaged again and seeded into T-225 flasks at 1.8 x 10^6/ml in 80 mls of medium.

HMVEC Cell Treatment for RNA isolation

Subconfluent (90% confluent) T-225 flasks of HMVEC were adjusted to 40 ml of medium per flask by removing excess medium. HMVEC were either left untreated (time 0) or treated with 10 ng/ml TNF-α for 1, 6 or 24 h. The medium was not changed at the time of TNF-α addition.

RNA isolation

At the designated time points, The flasks of HMVEC were trypsinized briefly to remove cells from the flasks and trypsinization was terminated by the addition of fetal calf serum. The cells were removed from the flasks and the flasks rinsed with PBS. The cells were pelleted, rinsed once in PBS and re-pelleted. The supernatant was removed and the cell pellet used for RNA isolation. Poly A+RNA was isolated directly using Fast Track 2.0™ (Invitrogen, Carlsbad, CA).

Construction of the Subtraction Library

The PCR-select cDNA subtraction kit™ (Clontech, Palo Alto, CA) was used to generate a subtraction library from untreated HMVEC poly A+ RNA (tester) and 1 h TNF-α-treated HMVEC poly A+ RNA (driver), according to the manufacturer's protocols. Ten secondary PCR reactions were combined and run on a 2% agarose gel. Fragments ranging from approximately 0.3kb – 10 kb were gel purified using the QIAgen gel extraction kit (QIAgen Inc., Valencia, CA) and inserted into the TA cloning vector, pCR2.1 (Invitrogen). TOP10F' competent *E. coli* (Invitrogen) were transformed and plated on LB plates containing 50 micrograms/ml ampicillin. Clones were isolated and grown in LB broth containing similar concentrations of ampicillin. Plasmids were sequenced using methods known in the art or described elsewhere herein.

As referenced above, the methods utilized for constructing the subtraction library followed the PCR-Select cDNA Subtraction Kit (Clonetech; Protocol # PT1117-1; Version # PR85431) which is hereby incorporated herein by reference in its entirety. Additional references to this method may be found in Diatchenko, L., et al., PNAS 93:6025-6030 (1996), which is hereby incorporated herein by reference in its entirety.

Example7 – Method of Cloning RET31 of the Present Invention.

A clone containing the predicted coding sequence of RET31 was isolated from human microvascular endothelial cells (HMVECs) treated with tumor necrosis factor alpha (TNFα) for 6 hours using reverse transcription/polymerase chain reaction (RT/PCR). RNA was purified from the TNFa stimulated HMVEC cells according to methods known in the art. A primer set (each at 400 nM final concentration) was used to amplify a 3 kb sequence using the following primers and conditions:

primer JNF388: CACACCACCATTACATCATCGTGGC (SEQ ID NO:145)
primer JNF525: TGCTGCTCTGCTACCAACCC (SEQ ID NO:146)

with 200 μM dNTP's, 1X Advantage 2 polymerase, and 2.0 μl DNA in 25.0 μl reaction. The experiment was cycled 35 times through the following sequence: ; 94°C for 30 sec, 68°C for 30 sec. then 72°C for 3.5 min. At the completion of the reaction, 6.0μl of loading dye was added and the entire reaction was separated by gel electrophoresis in a 1.2% agarose gel containing ethidium bromide. An ~3 kb size band was excised from the gel and purified using the QIAgen extraction kit (QIAgen, Valencia, CA). This fragment was ligated into the pTAdv cloning vector (Clontech, Palo Alto, CA) and sequenced using standard methods. The RET31 clone (SEQ ID NO:108; Figures 13A-F) contains about a 3 kb sequence corresponding to nucleotides 472 to 3513 of the predicted RET31 coding sequence (SEQ ID NO:147). The predicted RET31 coding sequence (SEQ ID NO:147) was derived from Incyte gene cluster 1026659.7.

A nucleic acid sequence corresponding to the nucleic acid sequence encoding the RET31 polypeptide was first identified in a subtraction library from TNF-α stimulated human lung microvascular endothelial cells (HMVEC). This subtraction clone sequence encoded a 408bp partial cDNA sequence, as shown:

RET31 subtraction clone

ACAATGGAGTGGCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAATTAAAGAAGGA
GGTGGGAAAAGAGGACTTATTGTTGTCATGGCCCATGAGATGATTGGAACTCAAATTGTTACTG
AGAGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATT
TGTGGAATACAATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGC
GAAGGTTGCAACAGGACAAAGTGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGT
TGACATTGATTGCAGTCAGAAGGTTGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCTCTCTCT
CTTCAGACTGTTTTCTCACTGT (SEQ ID NO:115)

Example 8 – Method of Determining the mRNA Expression Profile of RET31 Using Northern Hybridization.

Multiple tissue northern blots (MTN) were purchased from Clontech Laboratories (Palo Alto, CA) and hybridized with P^{32}-labeled RET31. Briefly, a 408 bp RET31 fragment (RET31/RsaI) was

isolated from subtraction clone 1hrTNF031 (SEQ ID NO:115) using RsaI restriction endonuclease, run on a 2.0% agarose gel, and purified using the QIAgen Gel Extraction Kit (QIAgen, Valencia, CA). Approximately 30 ng of RET31/RsaI was radiolabeled (6000Ci/mmol P^{32}-dCTP) using the Random Primed DNA Labeling Kit (Roche, Indianapolis, IN). Unincorporated nucleotides were removed using NucTrap Probe Purification Columns (Stratgene, La Jolla, CA). Radiolabeled RET31/RsaI probe was added at a specific activity of $1.5x10^6$ cpm/ml of ExpressHyb hybridization solution (Clontech) and incubated overnight at 65°C. Blots were washed to 2.0XSSC/0.05%SDS at 50°C and exposed to film for 24 and 48 h. The MTN's used were human MTN (#7760-1), human MTN II (#7759-1), human MTN III (#7767-1), and human cancer cell line MTN (#7757-1).

The results show the RET31 polypeptide was expressed predominately in adrenal gland, testis, and skeletal muscle; to a significant extent, in the liver, prostate ovary, and to a lesser extent, in placenta, pancreas, thymus, small intestine, thyroid, heart, kidney and liver (see Figure 15).

Example 9 – Method of Assessing The Affect of TNF-alpha on RET31 mRNA Expression.

In an effort to confirm the TNF-alpha dependent regulation of RET31 expression, HMVEC cells were treated with TNF-alpha over several time periods and the mRNA subsequently harvested and probed by northern hybridization. Briefly, untreated HMVEC, 1h TNF-α stimulated HMVEC, 6 h TNF-α stimulated HMVEC, 24h TNF-α stimulated HMVEC poly A+RNA (2 μg each) were run on a 1.2% agarose gel containing 3.0% formaldehyde and transferred to Hybond N+ nucleic acid transfer membrane (Amersham, Piscataway, NJ) using standard blotting techniques (see Maniatis et al. referenced herein). Membranes were auto cross-linked using Stratalinker (Stratagene) and prehybridized in ExpressHyb hybridization solution for 1 h and probed in parallel with the multiple tissue northern blots.

After hybridization, membranes were washed by continuous shaking for 30 minutes with low stringency solution (2XSSC/0.05%SDS) at room temperature with 2 changes of solution. Membranes were then washed for 30 minutes with high stringency solution (0.1XSSC/0.1%SDS) at 50°C with 1 change of solution. The membranes were exposed with intensifying screens to X-ray film at -70°C for 10 days.

The endothelial cell blot was reprobed for E-selectin and GAPDH.

The results confirmed RET31 is up-regulated by TNF-α, reaching a peak of expression at 6 h by northern blot analysis (see Figure 18).

~~Example 6~~Example 10 – **Method Of Assessing The Physiological Function Of The human phosphatase Polypeptide At The Cellular Level.**

The physiological function of the human phosphatase polypeptide may be assessed by expressing the sequences encoding human phosphatase at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression (examples are provided elsewhere herein). Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10, ug of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2ug of an additional plasmid containing sequences encoding a marker protein are cotransfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of human phosphatase polypeptides on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding human phosphatase and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods

well known by those of skill in the art. Expression of mRNA encoding human phosphatase polypeptides and other genes of interest can be analyzed by northern analysis or microarray techniques.

~~Example 7~~Example 11 – Method Of Screening For Compounds That Interact With The human phosphatase Polypeptide.

The following assays are designed to identify compounds that bind to the human phosphatase polypeptide, bind to other cellular proteins that interact with the human phosphatase polypeptide, and to compounds that interfere with the interaction of the human phosphatase polypeptide with other cellular proteins.

Such compounds can include, but are not limited to, other cellular proteins. Specifically, such compounds can include, but are not limited to, peptides, such as, for example, soluble peptides, including, but not limited to Ig-tailed fusion peptides, comprising extracellular portions of human phosphatase polypeptide transmembrane receptors, and members of random peptide libraries (see, e.g., Lam, K. S. et al., 1991, Nature 354:82-84; Houghton, R. et al., 1991, Nature 354:84-86), made of D-and/or L-configuration amino acids, phosphopeptides (including, but not limited to, members of random or partially degenerate phosphopeptide libraries; see, e.g., Songyang, Z., et al., 1993, Cell 72:767-778), antibodies (including, but not limited to, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and FAb, F(ab').sub.2 and FAb expression libary fragments, and epitope-binding fragments thereof), and small organic or inorganic molecules.

Compounds identified via assays such as those described herein can be useful, for example, in elaborating the biological function of the human phosphatase polypeptide, and for ameliorating symptoms of tumor progression, for example. In instances, for example, whereby a tumor progression state or disorder results from a lower overall level of human phosphatase expression, human phosphatase polypeptide, and/or human phosphatase polypeptide activity in a cell involved in the tumor progression state or disorder, compounds that interact with the human phosphatase polypeptide can include ones which accentuate or amplify the activity of the bound human phosphatase polypeptide. Such compounds would bring about an effective increase in the level of human phosphatase polypeptide activity, thus ameliorating symptoms of the tumor progression disorder or state. In instances whereby mutations within the human phosphatase polypeptide cause aberrant human phosphatase polypeptides to be made which have a deleterious effect that leads to

tumor progression, compounds that bind human phosphatase polypeptide can be identified that inhibit the activity of the bound human phosphatase polypeptide. Assays for testing the effectiveness of such compounds are known in the art and discussed, elsewhere herein.

~~Example 8~~Example 12 – Method Of Screening, In Vitro, Compounds That Bind To The Human Phosphatase Polypeptide.

In vitro systems can be designed to identify compounds capable of binding the human phosphatase polypeptide of the invention. Compounds identified can be useful, for example, in modulating the activity of wild type and/or mutant human phosphatase polypeptide, preferably mutant human phosphatase polypeptide, can be useful in elaborating the biological function of the human phosphatase polypeptide, can be utilized in screens for identifying compounds that disrupt normal human phosphatase polypeptide interactions, or can in themselves disrupt such interactions.

The principle of the assays used to identify compounds that bind to the human phosphatase polypeptide involves preparing a reaction mixture of the human phosphatase polypeptide and the test compound under conditions and for a time sufficient to allow the two components to interact and bind, thus forming a complex which can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways. For example, one method to conduct such an assay would involve anchoring human phosphatase polypeptide or the test substance onto a solid phase and detecting human phosphatase polypeptide /test compound complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, the human phosphatase polypeptide can be anchored onto a solid surface, and the test compound, which is not anchored, can be labeled, either directly or indirectly.

In practice, microtitre plates can conveniently be utilized as the solid phase. The anchored component can be immobilized by non-covalent or covalent attachments. Non-covalent attachment can be accomplished by simply coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein to be immobilized can be used to anchor the protein to the solid surface. The surfaces can be prepared in advance and stored.

In order to conduct the assay, the nonimmobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain

immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously nonimmobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the immobilized component (the antibody, in turn, can be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

Alternatively, a reaction can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for human phosphatase polypeptide or the test compound to anchor any complexes formed in solution, and a labeled antibody specific for the other component of the possible complex to detect anchored complexes.

~~Example 9~~Example 13 – Method Of Identifying Compounds That Interfere With Human Phosphatase Polypeptide/Cellular Product Interaction.

The human phosphatase polypeptide of the invention can, in vivo, interact with one or more cellular or extracellular macromolecules, such as proteins. Such macromolecules include, but are not limited to, polypeptides, particularly ligands, and those products identified via screening methods described, elsewhere herein. For the purposes of this discussion, such cellular and extracellular macromolecules are referred to herein as "binding partner(s)". For the purpose of the present invention, "binding partner" may also encompass polypeptides, small molecule compounds, polysaccarides, lipids, and any other molecule or molecule type referenced herein. Compounds that disrupt such interactions can be useful in regulating the activity of the human phosphatase polypeptide, especially mutant human phosphatase polypeptide. Such compounds can include, but are not limited to molecules such as antibodies, peptides, and the like described in elsewhere herein.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the human phosphatase polypeptide and its cellular or extracellular binding partner or partners involves preparing a reaction mixture containing the human phosphatase polypeptide, and the binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus forming a complex. In order to test a compound for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test

compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of human phosphatase polypeptide and its cellular or extracellular binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the human phosphatase polypeptide and the cellular or extracellular binding partner is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the human phosphatase polypeptide and the interactive binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal human phosphatase polypeptide can also be compared to complex formation within reaction mixtures containing the test compound and mutant human phosphatase polypeptide. This comparison can be important in those cases wherein it is desirable to identify compounds that disrupt interactions of mutant but not normal human phosphatase polypeptide.

The assay for compounds that interfere with the interaction of the human phosphatase polypeptide and binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the human phosphatase polypeptide or the binding partner onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the human phosphatase polypeptide and the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the human phosphatase polypeptide and interactive cellular or extracellular binding partner. Alternatively, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are described briefly below.

In a heterogeneous assay system, either the human phosphatase polypeptide or the interactive cellular or extracellular binding partner, is anchored onto a solid surface, while the non-anchored species is labeled, either directly or indirectly. In practice, microtitre plates are conveniently utilized. The anchored species can be immobilized by non-covalent or covalent attachments. Non-covalent attachment can be accomplished simply by coating the solid surface with a solution of the human

phosphatase polypeptide or binding partner and drying. Alternatively, an immobilized antibody specific for the species to be anchored can be used to anchor the species to the solid surface. The surfaces can be prepared in advance and stored.

In order to conduct the assay, the partner of the immobilized species is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the human phosphatase polypeptide and the interactive cellular or extracellular binding partner product is prepared in which either the human phosphatase polypeptide or their binding partners are labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Pat. No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt human phosphatase polypeptide -cellular or extracellular binding partner interaction can be identified.

In a particular embodiment, the human phosphatase polypeptide can be prepared for immobilization using recombinant DNA techniques known in the art. For example, the human

phosphatase polypeptide coding region can be fused to a glutathione-S-transferase (GST) gene using a fusion vector such as pGEX-5X-1, in such a manner that its binding activity is maintained in the resulting fusion product. The interactive cellular or extracellular product can be purified and used to raise a monoclonal antibody, using methods routinely practiced in the art and described above. This antibody can be labeled with the radioactive isotope .sup.125 I, for example, by methods routinely practiced in the art. In a heterogeneous assay, e.g., the GST- human phosphatase polypeptide fusion product can be anchored to glutathione-agarose beads. The interactive cellular or extracellular binding partner product can then be added in the presence or absence of the test compound in a manner that allows interaction and binding to occur. At the end of the reaction period, unbound material can be washed away, and the labeled monoclonal antibody can be added to the system and allowed to bind to the complexed components. The interaction between the human phosphatase polypeptide and the interactive cellular or extracellular binding partner can be detected by measuring the amount of radioactivity that remains associated with the glutathione-agarose beads. A successful inhibition of the interaction by the test compound will result in a decrease in measured radioactivity.

Alternatively, the GST- human phosphatase polypeptide fusion product and the interactive cellular or extracellular binding partner product can be mixed together in liquid in the absence of the solid glutathione-agarose beads. The test compound can be added either during or after the binding partners are allowed to interact. This mixture can then be added to the glutathione-agarose beads and unbound material is washed away. Again the extent of inhibition of the binding partner interaction can be detected by adding the labeled antibody and measuring the radioactivity associated with the beads.

In another embodiment of the invention, these same techniques can be employed using peptide fragments that correspond to the binding domains of the human phosphatase polypeptide product and the interactive cellular or extracellular binding partner (in case where the binding partner is a product), in place of one or both of the full length products.

Any number of methods routinely practiced in the art can be used to identify and isolate the protein's binding site. These methods include, but are not limited to, mutagenesis of one of the genes encoding one of the products and screening for disruption of binding in a co-immunoprecipitation assay. Compensating mutations in the gene encoding the second species in the complex can be selected. Sequence analysis of the genes encoding the respective products will reveal the mutations that correspond to the region of the product involved in interactive binding. Alternatively, one

product can be anchored to a solid surface using methods described in this Section above, and allowed to interact with and bind to its labeled binding partner, which has been treated with a proteolytic enzyme, such as trypsin. After washing, a short, labeled peptide comprising the binding domain can remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the cellular or extracellular binding partner product is obtained, short gene segments can be engineered to express peptide fragments of the product, which can then be tested for binding activity and purified or synthesized.

~~Example 10~~Example 14 - Isolation Of A Specific Clone From The Deposited Sample.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table I for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table I. Typically, each ATCC deposit sample cited in Table I comprises a mixture of approximately equal amounts (by weight) of about 1-10 plasmid DNAs, each containing a different cDNA clone and/or partial cDNA clone; but such a deposit sample may include plasmids for more or less than 2 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNA(s) cited for that clone in Table I. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:149, 151, 7, 9, 41, or 108.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with 32P-(-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:149, 151, 7, 9, 41, or 108 (i.e., within the region of SEQ ID NO:149, 151, 7, 9, 41, or 108 bounded by the 5′ NT and the 3′ NT of the clone defined in Table I) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 ul of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl2, 0.01% (w/v) gelatin, 20 uM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94 degree C for 1 min; annealing at 55 degree C for 1 min; elongation at 72 degree C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

~~Example 11~~Example 15 - **Tissue Distribution Of Polypeptide.**

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 10 is labeled with p32 using the rediprime ™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN0-100 column (Clontech Laboratories, Inc.) according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various tissues for mRNA expression.

Tissue Northern blots containing the bound mRNA of various tissues are examined with the labeled probe using ExpressHybtm hybridization solution (Clonetech according to manufacturers protocol number PT1190-1. Northern blots can be produced using various protocols well known in the art (e.g., Sambrook et al). Following hybridization and washing, the blots are mounted and exposed to film at –70C overnight, and the films developed according to standard procedures.

~~Example 12~~Example 16 - **Chromosomal Mapping Of The Polynucleotides.**

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:149, 151, 7, 9, 41, or 108. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions: 30 seconds,95 degree

C; 1 minute, 56 degree C; 1 minute, 70 degree C. This cycle is repeated 32 times followed by one 5 minute cycle at 70 degree C. Mammalian DNA, preferably human DNA, is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions are analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

~~Example 13~~Example 17 - Bacterial Expression Of A Polypeptide.

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 10, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Ampr), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, that expresses the lacI repressor and also confers kanamycin resistance (Kanr). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.600) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring

for 3-4 hours at 4 degree C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., supra). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., supra).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4 degree C or frozen at -80 degree C.

~~Example 14~~Example 18 - Purification Of A Polypeptide From An Inclusion Body.

The following alternative method can be used to purify a polypeptide expressed in E coli when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10 degree C.

Upon completion of the production phase of the E. coli fermentation, the cell culture is cooled to 4-10 degree C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4 degree C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4 degree C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 um membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perceptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perceptive Biosystems) and weak anion (Poros CM-20, Perceptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A280 monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Coomassie blue stained 16% SDS-PAGE gel when 5 ug of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

~~Example 15~~Example 19 - **Cloning And Expression Of A Polypeptide In A Baculovirus Expression System.**

In this example, the plasmid shuttle vector pAc373 is used to insert a polynucleotide into a baculovirus to express a polypeptide. A typical baculovirus expression vector contains the strong polyhedrin promoter of the Autographa californica nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites, which may include, for example BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is often used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from E. coli under control of a weak Drosophila promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pVL941 and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 10, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites at the 5' end of the primers in order to clone the amplified product into the expression vector. Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified elsewhere herein (if applicable), is amplified using the PCR protocol described in Example 10. If the naturally occurring signal sequence is used to produce the protein, the vector used does not need a second signal peptide. Alternatively, the vector can be modified to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. E. coli HB101 or other suitable E. coli hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five ug of a plasmid containing the polynucleotide is co-transformed with 1.0 ug of a commercially available linearized baculovirus DNA ("BaculoGoldtm baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One ug of BaculoGoldtm virus DNA and 5ug of the plasmid are mixed in a sterile well of a microtiter plate containing 50ul of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 ul Lipofectin plus 90 ul Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27 degrees C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27 degrees C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, supra. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip

of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 ul of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4 degree C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 uCi of 35S-methionine and 5 uCi 35S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

~~Example 16~~Example 20 - Expression Of A Polypeptide In Mammalian Cells.

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse

NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transformation with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transformed cells.

The transformed gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

A polynucleotide of the present invention is amplified according to the protocol outlined in herein. If the naturally occurring signal sequence is used to produce the protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.) The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. E. coli HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transformation. Five μg of an expression plasmid is cotransformed with 0.5 ug of the plasmid pSVneo using lipofectin (Felgner et al., supra). The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are

trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 uM, 2 uM, 5 uM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 uM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

~~Example 17~~Example 21 - Protein Fusions.

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example described herein; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the half-life time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

The naturally occurring signal sequence may be used to produce the protein (if applicable). Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891 and/or US Patent No. 6,066,781, supra.)

Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCCACCGTGCCCAG
CACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC
CTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGTGGACGTAAGCCACGAAGA
CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCT
CCCAACCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG
CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT
CTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCC
GGGTAAATGAGTGCGACGGCCGCGACTCTAGAGGAT (SEQ ID NO:76)

~~Example 18~~Example 22 - Production Of An Antibody From A Polypeptide.

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing a polypeptide of the present invention are administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified

Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56 degrees C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 ug/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody that binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones that produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')2 and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Moreover, in another preferred method, the antibodies directed against the polypeptides of the present invention may be produced in plants. Specific methods are disclosed in US Patent Nos. 5,959,177, and 6,080,560, which are hereby incorporated in their entirety herein. The methods not only describe methods of expressing antibodies, but also the means of assembling foreign multimeric proteins in plants (i.e., antibodies, etc,), and the subsequent secretion of such antibodies from the plant.

~~Example 19~~Example 23 - Regulation of Protein Expression Via Controlled Aggregation In The Endoplasmic Reticulum.

As described more particularly herein, proteins regulate diverse cellular processes in higher organisms, ranging from rapid metabolic changes to growth and differentiation. Increased production of specific proteins could be used to prevent certain diseases and/or disease states. Thus, the ability to modulate the expression of specific proteins in an organism would provide significant benefits.

Numerous methods have been developed to date for introducing foreign genes, either under the control of an inducible, constitutively active, or endogenous promoter, into organisms. Of particular interest are the inducible promoters (see, M. Gossen, et al., Proc. Natl. Acad. Sci. USA., 89:5547 (1992); Y. Wang, et al., Proc. Natl. Acad. Sci. USA, 91:8180 (1994), D. No., et al., Proc. Natl. Acad. Sci. USA, 93:3346 (1996); and V.M. Rivera, et al., Nature Med, 2:1028 (1996); in addition to additional examples disclosed elsewhere herein). In one example, the gene for erthropoietin (Epo) was transferred into mice and primates under the control of a small molecule inducer for expression (e.g., tetracycline or rapamycin) (see, D. Bohl, et al., Blood, 92:1512, (1998); K.G. Rendahl, et al., Nat. Biotech, 16:757, (1998); V.M. Rivera, et al., Proc. Natl. Acad. Sci. USA, 96:8657 (1999); and X.Ye et al., Science, 283:88 (1999). Although such systems enable efficient induction of the gene of interest in the organism upon addition of the inducing agent (i.e., tetracycline, rapamycin, etc,.), the levels of expression tend to peak at 24 hours and trail off to background levels after 4 to 14 days. Thus, controlled transient expression is virtually impossible using these systems, though such control would be desirable.

A new alternative method of controlling gene expression levels of a protein from a transgene (i.e., includes stable and transient transformants) has recently been elucidated (V.M. Rivera., et al., Science, 287:826-830, (2000)). This method does not control gene expression at the level of the

mRNA like the aforementioned systems. Rather, the system controls the level of protein in an active secreted form. In the absence of the inducing agent, the protein aggregates in the ER and is not secreted. However, addition of the inducing agent results in dis-aggregation of the protein and the subsequent secretion from the ER. Such a system affords low basal secretion, rapid, high level secretion in the presence of the inducing agent, and rapid cessation of secretion upon removal of the inducing agent. In fact, protein secretion reached a maximum level within 30 minutes of induction, and a rapid cessation of secretion within 1 hour of removing the inducing agent. The method is also applicable for controlling the level of production for membrane proteins.

Detailed methods are presented in V.M. Rivera., et al., Science, 287:826-830, (2000)), briefly:

Fusion protein constructs are created using polynucleotide sequences of the present invention with one or more copies (preferably at least 2, 3, 4, or more) of a conditional aggregation domain (CAD) a domain that interacts with itself in a ligand-reversible manner (i.e., in the presence of an inducing agent) using molecular biology methods known in the art and discussed elsewhere herein. The CAD domain may be the mutant domain isolated from the human FKBP12 (Phe^{36} to Met) protein (as disclosed in V.M. Rivera., et al., Science, 287:826-830, (2000), or alternatively other proteins having domains with similar ligand-reversible, self-aggregation properties. As a principle of design the fusion protein vector would contain a furin cleavage sequence operably linked between the polynucleotides of the present invention and the CAD domains. Such a cleavage site would enable the proteolytic cleavage of the CAD domains from the polypeptide of the present invention subsequent to secretion from the ER and upon entry into the trans-Golgi (J.B. Denault, et al., FEBS Lett., 379:113, (1996)). Alternatively, the skilled artisan would recognize that any proteolytic cleavage sequence could be substituted for the furin sequence provided the substituted sequence is cleavable either endogenously (e.g., the furin sequence) or exogenously (e.g., post secretion, post purification, post production, etc.). The preferred sequence of each feature of the fusion protein construct, from the 5' to 3' direction with each feature being operably linked to the other, would be a promoter, signal sequence, "X" number of (CAD)x domains, the furin sequence (or other proteolytic sequence), and the coding sequence of the polypeptide of the present invention. The artisan would appreciate that the promotor and signal sequence, independent from the other, could be either the endogenous promotor or signal sequence of a polypeptide of the present invention, or alternatively, could be a heterologous signal sequence and promotor.

The specific methods described herein for controlling protein secretion levels through controlled ER aggregation are not meant to be limiting are would be generally applicable to any of the polynucleotides and polypeptides of the present invention, including variants, homologues, orthologs, and fragments therein.

~~Example 20~~Example 24 - Alteration Of Protein Glycosylation Sites to Enhance Characteristics Of Polypeptides Of The Invention.

Many eukaryotic cell surface and proteins are post-translationally processed to incorporate N-linked and O-linked carbohydrates (Kornfeld and Kornfeld (1985) Annu. Rev. Biochem. 54:631-64; Rademacher et al., (1988) Annu. Rev. Biochem. 57:785-838). Protein glycosylation is thought to serve a variety of functions including: augmentation of protein folding, inhibition of protein aggregation, regulation of intracellular trafficking to organelles, increasing resistance to proteolysis, modulation of protein antigenicity, and mediation of intercellular adhesion (Fieldler and Simons (1995) Cell, 81:309-312; Helenius (1994) Mol. Biol. Of the Cell 5:253-265; Olden et al., (1978) Cell, 13:461-473; Caton et al., (1982) Cell, 37:417-427; Alexamnder and Elder (1984), Science, 226:1328-1330; and Flack et al., (1994), J. Biol. Chem., 269:14015-14020). In higher organisms, the nature and extent of glycosylation can markedly affect the circulating half-life and bio-availability of proteins by mechanisms involving receptor mediated uptake and clearance (Ashwell and Morrell, (1974), Adv. Enzymol., 41:99-128; Ashwell and Harford (1982), Ann. Rev. Biochem., 51:531-54). Receptor systems have been identified that are thought to play a major role in the clearance of serum proteins through recognition of various carbohydrate structures on the glycoproteins (Stockert (1995), Physiol. Rev., 75:591-609; Kery et al., (1992), Arch. Biochem. Biophys., 298:49-55). Thus, production strategies resulting in incomplete attachment of terminal sialic acid residues might provide a means of shortening the bioavailability and half-life of glycoproteins. Conversely, expression strategies resulting in saturation of terminal sialic acid attachment sites might lengthen protein bioavailability and half-life.

In the development of recombinant glycoproteins for use as pharmaceutical products, for example, it has been speculated that the pharmacodynamics of recombinant proteins can be modulated by the addition or deletion of glycosylation sites from a glycoproteins primary structure (Berman and Lasky (1985a) Trends in Biotechnol., 3:51-53). However, studies have reported that the deletion of N-linked glycosylation sites often impairs intracellular transport and results in the

intracellular accumulation of glycosylation site variants (Machamer and Rose (1988), J. Biol Chem., 263:5955-5960; Gallagher et al., (1992), J. Virology., 66:7136-7145; Collier et al., (1993), Biochem., 32:7818-7823; Claffey et al., (1995) Biochemica et Biophysica Acta, 1246:1-9; Dube et al., (1988), J. Biol. Chem. 263:17516-17521). While glycosylation site variants of proteins can be expressed intracellularly, it has proved difficult to recover useful quantities from growth conditioned cell culture medium.

Moreover, it is unclear to what extent a glycosylation site in one species will be recognized by another species glycosylation machinery. Due to the importance of glycosylation in protein metabolism, particularly the secretion and/or expression of the protein, whether a glycosylation signal is recognized may profoundly determine a proteins ability to be expressed, either endogenously or recombinately, in another organism (i.e., expressing a human protein in E.coli, yeast, or viral organisms; or an E.coli, yeast, or viral protein in human, etc.). Thus, it may be desirable to add, delete, or modify a glycosylation site, and possibly add a glycosylation site of one species to a protein of another species to improve the proteins functional, bioprocess purification, and/or structural characteristics (e.g., a polypeptide of the present invention).

A number of methods may be employed to identify the location of glycosylation sites within a protein. One preferred method is to run the translated protein sequence through the PROSITE computer program (Swiss Institute of Bioinformatics). Once identified, the sites could be systematically deleted, or impaired, at the level of the DNA using mutagenesis methodology known in the art and available to the skilled artisan, Preferably using PCR-directed mutagenesis (See Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982)). Similarly, glycosylation sites could be added, or modified at the level of the DNA using similar methods, preferably PCR methods (See, Maniatis, supra). The results of modifying the glycosylation sites for a particular protein (e.g., solubility, secretion potential, activity, aggregation, proteolytic resistance, etc.) could then be analyzed using methods know in the art.

The skilled artisan would acknowledge the existence of other computer algorithms capable of predicting the location of glycosylation sites within a protein. For example, the Motif computer program (Genetics Computer Group suite of programs) provides this function, as well.

~~Example 21~~Example 25 - Method Of Enhancing The Biological Activity/Functional Characteristics Of Invention Through Molecular Evolution.

Although many of the most biologically active proteins known are highly effective for their specified function in an organism, they often possess characteristics that make them undesirable for transgenic, therapeutic, and/or industrial applications. Among these traits, a short physiological half-life is the most prominent problem, and is present either at the level of the protein, or the level of the proteins mRNA. The ability to extend the half-life, for example, would be particularly important for a proteins use in gene therapy, transgenic animal production, the bioprocess production and purification of the protein, and use of the protein as a chemical modulator among others. Therefore, there is a need to identify novel variants of isolated proteins possessing characteristics which enhance their application as a therapeutic for treating diseases of animal origin, in addition to the proteins applicability to common industrial and pharmaceutical applications.

Thus, one aspect of the present invention relates to the ability to enhance specific characteristics of invention through directed molecular evolution. Such an enhancement may, in a non-limiting example, benefit the inventions utility as an essential component in a kit, the inventions physical attributes such as its solubility, structure, or codon optimization, the inventions specific biological activity, including any associated enzymatic activity, the proteins enzyme kinetics, the proteins Ki, Kcat, Km, Vmax, Kd, protein-protein activity, protein-DNA binding activity, antagonist/inhibitory activity (including direct or indirect interaction), agonist activity (including direct or indirect interaction), the proteins antigenicity (e.g., where it would be desirable to either increase or decrease the antigenic potential of the protein), the immunogenicity of the protein, the ability of the protein to form dimers, trimers, or multimers with either itself or other proteins, the antigenic efficacy of the invention, including its subsequent use a preventative treatment for disease or disease states, or as an effector for targeting diseased genes. Moreover, the ability to enhance specific characteristics of a protein may also be applicable to changing the characterized activity of an enzyme to an activity completely unrelated to its initially characterized activity. Other desirable enhancements of the invention would be specific to each individual protein, and would thus be well known in the art and contemplated by the present invention.

For example, an engineered phosphatase may be constitutively active. Alternatively, an engineered phosphatase may be constitutively active in the absence of ligand binding. In yet another example, an engineered phosphatase may be capable of being activated with less than all of the

regulatory factors and/or conditions typically required for phosphatase activation (e.g., ligand binding, phosphorylation, conformational changes, etc.). Alternatively, an engineered phosphatase may have altered substrate specificity. Such phosphatases would be useful in screens to identify phosphatase modulators, among other uses described herein.

Directed evolution is comprised of several steps. The first step is to establish a library of variants for the gene or protein of interest. The most important step is to then select for those variants that entail the activity you wish to identify. The design of the screen is essential since your screen should be selective enough to eliminate non-useful variants, but not so stringent as to eliminate all variants. The last step is then to repeat the above steps using the best variant from the previous screen. Each successive cycle, can then be tailored as necessary, such as increasing the stringency of the screen, for example.

Over the years, there have been a number of methods developed to introduce mutations into macromolecules. Some of these methods include, random mutagenesis, "error-prone" PCR, chemical mutagenesis, site-directed mutagenesis, and other methods well known in the art (for a comprehensive listing of current mutagenesis methods, see Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982)). Typically, such methods have been used, for example, as tools for identifying the core functional region(s) of a protein or the function of specific domains of a protein (if a multi-domain protein). However, such methods have more recently been applied to the identification of macromolecule variants with specific or enhanced characteristics.

Random mutagenesis has been the most widely recognized method to date. Typically, this has been carried out either through the use of "error-prone" PCR (as described in Moore, J., et al, Nature Biotechnology 14:458, (1996), or through the application of randomized synthetic oligonucleotides corresponding to specific regions of interest (as described by Derbyshire, K.M. et al, Gene, 46:145-152, (1986), and Hill, DE, et al, Methods Enzymol., 55:559-568, (1987). Both approaches have limits to the level of mutagenesis that can be obtained. However, either approach enables the investigator to effectively control the rate of mutagenesis. This is particularly important considering the fact that mutations beneficial to the activity of the enzyme are fairly rare. In fact, using too high a level of mutagenesis may counter or inhibit the desired benefit of a useful mutation.

While both of the aforementioned methods are effective for creating randomized pools of macromolecule variants, a third method, termed "DNA Shuffling", or "sexual PCR" (WPC,

Stemmer, PNAS, 91:10747, (1994)) has recently been elucidated. DNA shuffling has also been referred to as "directed molecular evolution", "exon-shuffling", "directed enzyme evolution", "in vitro evolution", and "artificial evolution". Such reference terms are known in the art and are encompassed by the invention. This new, preferred, method apparently overcomes the limitations of the previous methods in that it not only propagates positive traits, but simultaneously eliminates negative traits in the resulting progeny.

DNA shuffling accomplishes this task by combining the principal of in vitro recombination, along with the method of "error-prone" PCR. In effect, you begin with a randomly digested pool of small fragments of your gene, created by Dnase I digestion, and then introduce said random fragments into an "error-prone" PCR assembly reaction. During the PCR reaction, the randomly sized DNA fragments not only hybridize to their cognate strand, but also may hybridize to other DNA fragments corresponding to different regions of the polynucleotide of interest – regions not typically accessible via hybridization of the entire polynucleotide. Moreover, since the PCR assembly reaction utilizes "error-prone" PCR reaction conditions, random mutations are introduced during the DNA synthesis step of the PCR reaction for all of the fragments -further diversifying the potential hybridization sites during the annealing step of the reaction.

A variety of reaction conditions could be utilized to carry-out the DNA shuffling reaction. However, specific reaction conditions for DNA shuffling are provided, for example, in PNAS, 91:10747, (1994). Briefly:

Prepare the DNA substrate to be subjected to the DNA shuffling reaction. Preparation may be in the form of simply purifying the DNA from contaminating cellular material, chemicals, buffers, oligonucleotide primers, deoxynucleotides, RNAs, etc., and may entail the use of DNA purification kits as those provided by Qiagen, Inc., or by the Promega, Corp., for example.

Once the DNA substrate has been purified, it would be subjected to Dnase I digestion. About 2-4ug of the DNA substrate(s) would be digested with .0015 units of Dnase I (Sigma) per ul in 100ul of 50mM Tris-HCL, pH 7.4/1mM MgCl2 for 10-20 min. at room temperature. The resulting fragments of 10-50bp could then be purified by running them through a 2% low-melting point agarose gel by electrophoresis onto DE81 ion-exchange paper (Whatmann) or could be purified using Microcon concentrators (Amicon) of the appropriate molecular weight cutoff, or could use oligonucleotide purification columns (Qiagen), in addition to other methods known in the art. If

using DE81 ion-exchange paper, the 10-50bp fragments could be eluted from said paper using 1M NaCl, followed by ethanol precipitation.

The resulting purified fragments would then be subjected to a PCR assembly reaction by re-suspension in a PCR mixture containing: 2mM of each dNTP, 2.2mM MgCl2, 50 mM KCl, 10mM Tris•HCL, pH 9.0, and 0.1% Triton X-100, at a final fragment concentration of 10-30ng/ul. No primers are added at this point. *Taq* DNA polymerase (Promega) would be used at 2.5 units per 100ul of reaction mixture. A PCR program of 94 C for 60s; 94 C for 30s, 50-55 C for 30s, and 72 C for 30s using 30-45 cycles, followed by 72 C for 5min using an MJ Research (Cambridge, MA) PTC-150 thermocycler. After the assembly reaction is completed, a 1:40 dilution of the resulting primerless product would then be introduced into a PCR mixture (using the same buffer mixture used for the assembly reaction) containing 0.8um of each primer and subjecting this mixture to 15 cycles of PCR (using 94 C for 30s, 50 C for 30s, and 72 C for 30s). The referred primers would be primers corresponding to the nucleic acid sequences of the polynucleotide(s) utilized in the shuffling reaction. Said primers could consist of modified nucleic acid base pairs using methods known in the art and referred to else where herein, or could contain additional sequences (i.e., for adding restriction sites, mutating specific base-pairs, etc.).

The resulting shuffled, assembled, and amplified product can be purified using methods well known in the art (e.g., Qiagen PCR purification kits) and then subsequently cloned using appropriate restriction enzymes.

Although a number of variations of DNA shuffling have been published to date, such variations would be obvious to the skilled artisan and are encompassed by the invention. The DNA shuffling method can also be tailored to the desired level of mutagenesis using the methods described by Zhao, et al. (Nucl Acid Res., 25(6):1307-1308, (1997).

As described above, once the randomized pool has been created, it can then be subjected to a specific screen to identify the variant possessing the desired characteristic(s). Once the variant has been identified, DNA corresponding to the variant could then be used as the DNA substrate for initiating another round of DNA shuffling. This cycle of shuffling, selecting the optimized variant of interest, and then re-shuffling, can be repeated until the ultimate variant is obtained. Examples of model screens applied to identify variants created using DNA shuffling technology may be found in the following publications: J. C., Moore, et al., J. Mol. Biol., 272:336-347, (1997), F.R., Cross, et al., Mol. Cell. Biol., 18:2923-2931, (1998), and A. Crameri., et al., Nat. Biotech., 15:436-438, (1997).

DNA shuffling has several advantages. First, it makes use of beneficial mutations. When combined with screening, DNA shuffling allows the discovery of the best mutational combinations and does not assume that the best combination contains all the mutations in a population. Secondly, recombination occurs simultaneously with point mutagenesis. An effect of forcing DNA polymerase to synthesize full-length genes from the small fragment DNA pool is a background mutagenesis rate. In combination with a stringent selection method, enzymatic activity has been evolved up to 16000 fold increase over the wild-type form of the enzyme. In essence, the background mutagenesis yielded the genetic variability on which recombination acted to enhance the activity.

A third feature of recombination is that it can be used to remove deleterious mutations. As discussed above, during the process of the randomization, for every one beneficial mutation, there may be at least one or more neutral or inhibitory mutations. Such mutations can be removed by including in the assembly reaction an excess of the wild-type random-size fragments, in addition to the random-size fragments of the selected mutant from the previous selection. During the next selection, some of the most active variants of the polynucleotide/polypeptide/enzyme, should have lost the inhibitory mutations.

Finally, recombination enables parallel processing. This represents a significant advantage since there are likely multiple characteristics that would make a protein more desirable (e.g. solubility, activity, etc.). Since it is increasingly difficult to screen for more than one desirable trait at a time, other methods of molecular evolution tend to be inhibitory. However, using recombination, it would be possible to combine the randomized fragments of the best representative variants for the various traits, and then select for multiple properties at once.

DNA shuffling can also be applied to the polynucleotides and polypeptides of the present invention to decrease their immunogenicity in a specified host. For example, a particular variant of the present invention may be created and isolated using DNA shuffling technology. Such a variant may have all of the desired characteristics, though may be highly immunogenic in a host due to its novel intrinsic structure. Specifically, the desired characteristic may cause the polypeptide to have a non-native structure which could no longer be recognized as a "self" molecule, but rather as a "foreign", and thus activate a host immune response directed against the novel variant. Such a limitation can be overcome, for example, by including a copy of the gene sequence for a xenobiotic ortholog of the native protein in with the gene sequence of the novel variant gene in one or more cycles of DNA shuffling. The molar ratio of the ortholog and novel variant DNAs could be varied

accordingly. Ideally, the resulting hybrid variant identified would contain at least some of the coding sequence which enabled the xenobiotic protein to evade the host immune system, and additionally, the coding sequence of the original novel variant that provided the desired characteristics.

Likewise, the invention encompasses the application of DNA shuffling technology to the evolution of polynucleotides and polypeptides of the invention, wherein one or more cycles of DNA shuffling include, in addition to the gene template DNA, oligonucleotides coding for known allelic sequences, optimized codon sequences, known variant sequences, known polynucleotide polymorphism sequences, known ortholog sequences, known homologue sequences, additional homologous sequences, additional non-homologous sequences, sequences from another species, and any number and combination of the above.

In addition to the described methods above, there are a number of related methods that may also be applicable, or desirable in certain cases. Representative among these are the methods discussed in PCT applications WO 98/31700, and WO 98/32845, which are hereby incorporated by reference. Furthermore, related methods can also be applied to the polynucleotide sequences of the present invention in order to evolve invention for creating ideal variants for use in gene therapy, protein engineering, evolution of whole cells containing the variant, or in the evolution of entire enzyme pathways containing polynucleotides of the invention as described in PCT applications WO 98/13485, WO 98/13487, WO 98/27230, WO 98/31837, and Crameri, A., et al., Nat. Biotech., 15:436-438, (1997), respectively.

Additional methods of applying "DNA Shuffling" technology to the polynucleotides and polypeptides of the present invention, including their proposed applications, may be found in US Patent No. 5,605,793; PCT Application No. WO 95/22625; PCT Application No. WO 97/20078; PCT Application No. WO 97/35966; and PCT Application No. WO 98/42832; PCT Application No. WO 00/09727 specifically provides methods for applying DNA shuffling to the identification of herbicide selective crops which could be applied to the polynucleotides and polypeptides of the present invention; additionally, PCT Application No. WO 00/12680 provides methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that confer detectable phenotypic properties on plant species; each of the above are hereby incorporated in their entirety herein for all purposes.

~~Example 22~~Example 26 - Method Of Determining Alterations In A Gene Corresponding To A Polynucleotide.

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:149, 151, 7, 9, 41, or 108. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30 seconds; 60-120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe

are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

~~Example 23~~Example 27 - **Method Of Detecting Abnormal Levels Of A Polypeptide In Biological Sample.**

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described elsewhere herein. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

~~Example 24~~Example 28 – **Formulation.**

The invention also provides methods of treatment and/or prevention diseases, disorders, and/or conditions (such as, for example, any one or more of the diseases or disorders disclosed herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is

meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about 1ug/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a dose rate of about 1 ug/kg/hour to about 50 ug/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), bucally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), bucally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention may also be suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules), suitable hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., Id.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988).

Sustained-release Therapeutics also include liposomally entrapped Therapeutics of the invention (see, generally, Langer, Science 249:1527-1533 (1990); Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. (USA) 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci.(USA) 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal Therapeutic.

In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (see Langer, supra; Sefton, CRC Crit. Ref. Biomed. Eng. 14:201 (1987); Buchwald et al., Surgery 88:507 (1980); Saudek et al., N. Engl. J. Med. 321:574 (1989)).

Other controlled release systems are discussed in the review by Langer (Science 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation.

For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to the Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The Therapeutic will typically be formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any pharmaceutical used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutics generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Therapeutics ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized Therapeutic using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the Therapeutics of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other therapeutic compounds.

The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment, Therapeutics of the invention are administered in combination with alum. In another specific embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be administered with the Therapeutics of the invention include, but are not limited to, vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diptheria, hepatitis A, hepatitis B, haemophilus influenzae B, whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

The Therapeutics of the invention may be administered alone or in combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents, cytokines and/or growth factors. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or

sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In one embodiment, the Therapeutics of the invention are administered in combination with members of the TNF family. TNF, TNF-related or TNF-like molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokine-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-IBB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892),TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153.

In certain embodiments, Therapeutics of the invention are administered in combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR(zidovudine/AZT), VIDEX(didanosine/ddI), HIVID(zalcitabine/ddC), ZERIT(stavudine/d4T), EPIVIR(lamivudine/3TC), and COMBIVIR(zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, VIRAMUNE(nevirapine), RESCRIPTOR(delavirdine), and SUSTIVA(efavirenz). Protease inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, CRIXIVAN(indinavir), NORVIR(ritonavir), INVIRASE(saquinavir), and VIRACEPT(nelfinavir).

In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with Therapeutics of the invention to treat AIDS and/or to prevent or treat HIV infection.

In other embodiments, Therapeutics of the invention may be administered in combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE, DAPSONE, PENTAMIDINE, ATOVAQUONE, ISONIAZID, RIFAMPIN, PYRAZINAMIDE, ETHAMBUTOL, RIFABUTIN, CLARITHROMYCIN, AZITHROMYCIN, GANCICLOVIR, FOSCARNET, CIDOFOVIR, FLUCONAZOLE, ITRACONAZOLE, KETOCONAZOLE, ACYCLOVIR, FAMCICOLVIR, PYRIMETHAMINE, LEUCOVORIN, NEUPOGEN (filgrastim/G-CSF), and LEUKINE((sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE, DAPSONE, PENTAMIDINE, and/or ATOVAQUONE(to prophylactically treat or prevent an opportunistic Pneumocystis carinii pneumonia infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ISONIAZID, RIFAMPIN, PYRAZINAMIDE, and/or ETHAMBUTOL to prophylactically treat or prevent an opportunistic Mycobacterium avium complex infection. In another specific embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN, CLARITHROMYCIN, and/or AZITHROMYCIN to prophylactically treat or prevent an opportunistic Mycobacterium tuberculosis infection. In another specific embodiment, Therapeutics of the invention are used in any combination with GANCICLOVIR, FOSCARNET, and/or CIDOFOVIR to prophylactically treat or prevent an opportunistic cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE, ITRACONAZOLE, and/or KETOCONAZOLE to prophylactically treat or prevent an opportunistic fungal infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ACYCLOVIR and/or FAMCICOLVIR to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE and/or LEUCOVORIN to prophylactically treat or prevent an opportunistic Toxoplasma gondii infection. In another specific embodiment, Therapeutics of the invention are

used in any combination with LEUCOVORIN and/or NEUPOGEN to prophylactically treat or prevent an opportunistic bacterial infection.

In a further embodiment, the Therapeutics of the invention are administered in combination with an antiviral agent. Antiviral agents that may be administered with the Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

In a further embodiment, the Therapeutics of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with the Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamthoxazole, and vancomycin.

Conventional nonspecific immunosuppressive agents, that may be administered in combination with the Therapeutics of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by suppressing the function of responding T cells.

In specific embodiments, Therapeutics of the invention are administered in combination with immunosuppressants. Immunosuppressants preparations that may be administered with the Therapeutics of the invention include, but are not limited to, ORTHOCLONE((OKT3), SANDIMMUNE/NEORAL/SANGDYA(cyclosporin), PROGRAF(tacrolimus), CELLCEPT(mycophenolate), Azathioprine, glucorticosteroids, and RAPAMUNE(sirolimus). In a specific embodiment, immunosuppressants may be used to prevent rejection of organ or bone marrow transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone or in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the Therapeutics of the invention include, but not limited to, GAMMAR, IVEEGAM, SANDOGLOBULIN, GAMMAGARD S/D, and GAMIMUNE. In a specific embodiment, Therapeutics of the invention are administered in combination with intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow transplant).

In an additional embodiment, the Therapeutics of the invention are administered alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the Therapeutics of the invention include, but are not limited to, glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives, thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucolome, difenpiramide, ditazol, emorfazone, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline, perisoxal, pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compositions of the invention are administered in combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the Therapeutics of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptopurine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., mephalen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepa); steroids and combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

In a specific embodiment, formulations of the present invention may further comprise antagonists of P-glycoprotein (also referred to as the multiresistance protein, or PGP), including antagonists of its encoding polynucleotides (e.g., antisense oligonucleotides, ribozymes, zinc-finger proteins, etc.). P-glycoprotein is well known for decreasing the efficacy of various drug administrations due to its ability to export intracellular levels of absorbed drug to the cell exterior. While this activity has been particularly pronounced in cancer cells in response to the administration of chemotherapy regimens, a variety of other cell types and the administration of other drug classes have been noted (e.g., T-cells and anti-HIV drugs). In fact, certain mutations in the PGP gene significantly reduces PGP function, making it less able to force drugs out of cells. People who have

two versions of the mutated gene--one inherited from each parent--have more than four times less PGP than those with two normal versions of the gene. People may also have one normal gene and one mutated one. Certain ethnic populations have increased incidence of such PGP mutations. Among individuals from Ghana, Kenya, the Sudan, as well as African Americans, frequency of the normal gene ranged from 73% to 84%. In contrast, the frequency was 34% to 59% among British whites, Portuguese, Southwest Asian, Chinese, Filipino and Saudi populations. As a result, certain ethnic populations may require increased administration of PGP antagonist in the formulation of the present invention to arrive at the an efficacious dose of the therapeutic (e.g., those from African descent). Conversely, certain ethnic populations, particularly those having increased frequency of the mutated PGP (e.g., of Caucasian descent, or non-African descent) may require less pharmaceutical compositions in the formulation due to an effective increase in efficacy of such compositions as a result of the increased effective absorption (e.g., less PGP activity) of said composition.

Moreover, in another specific embodiment, formulations of the present invention may further comprise antagonists of OATP2 (also referred to as the multiresistance protein, or MRP2), including antagonists of its encoding polynucleotides (e.g., antisense oligonucleotides, ribozymes, zinc-finger proteins, etc.). The invention also further comprises any additional antagonists known to inhibit proteins thought to be attributable to a multidrug resistant phenotype in proliferating cells.

In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment, Therapeutics of the invention are administered with Rituxmab and CHOP, or Rituxmab and any combination of the components of CHOP.

In an additional embodiment, the Therapeutics of the invention are administered in combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

In an additional embodiment, the Therapeutics of the invention are administered in combination with angiogenic proteins. Angiogenic proteins that may be administered with the Therapeutics of the invention include, but are not limited to, Glioma Derived Growth Factor (GDGF), as disclosed in European Patent Number EP-399816; Platelet Derived Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet Derived Growth Factor-B (PDGF-B), as disclosed in European Patent Number EP-282317; Placental Growth Factor (PlGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PlGF-2), as disclosed in Hauser et al., Gorwth Factors, 4:259-268 (1993); Vascular Endothelial Growth Factor (VEGF), as disclosed in International Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2 (VEGF-2), as disclosed in International Publication Number WO 96/39515; Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/07832; and Vascular Endothelial Growth Factor-E (VEGF-E), as disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE((SARGRAMOSTIM() and NEUPOGEN((FILGRASTIM().

In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

In additional embodiments, the Therapeutics of the invention are administered in combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

~~Example 25~~Example 29 - Method Of Treating Decreased Levels Of The Polypeptide.

The present invention relates to a method for treating an individual in need of an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided herein.

~~Example 26~~Example 30 - Method Of Treating Increased Levels Of The Polypeptide.

The present invention also relates to a method of treating an individual in need of a decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and antibodies of the invention).

In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer. For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided herein.

~~Example 27~~Example 31 - Method Of Treatment Using Gene Therapy-Ex Vivo.

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37 degree C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 10 using primers and having appropriate restriction sites and initiation/stop codons, if necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

~~Example 28~~Example 32 - **Gene Therapy Using Endogenous Genes Corresponding To Polynucleotides Of The Invention.**

Another method of gene therapy according to the present invention involves operably associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA, 86:8932-8935 (1989); and Zijlstra et al., Nature, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of the polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or any other method known in the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na2 HPO4, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately 3X106 cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3'end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an Xba site at the 3'end; the other non-coding sequence (fragment 2) is amplified with a BamHI site at the 5'end and a HindIII site at the 3'end. The CMV promoter and the fragments (1 and

2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 µg/ml. 0.5 ml of the cell suspension (containing approximately 1.5.X106 cells) is then added to the cuvette, and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 µF and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a 10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product. The fibroblasts can then be introduced into a patient as described above.

~~Example 29~~Example 33 - Method Of Treatment Using Gene Therapy - In Vivo.

Another aspect of the present invention is using in vivo gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata et al., Cardiovasc. Res. 35(3):470-479 (1997); Chao et al., Pharmacol. Res. 35(6):517-522 (1997); Wolff, Neuromuscul. Disord. 7(5):314-318 (1997); Schwartz et al., Gene

Ther. 3(5):405-411 (1996); Tsurumi et al., Circulation 94(12):3281-3290 (1996) (incorporated herein by reference).

The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the present invention may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) Ann. NY Acad. Sci. 772:126-139 and Abdallah B. et al. (1995) Biol. Cell 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although

delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. In vivo muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle in vivo is determined as follows. Suitable template DNA for production of mRNA coding for polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after

preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be use to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA.

~~Example 30~~Example 34 - Transgenic Animals.

The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson et al., Appl. Microbiol. Biotechnol. 40:691-698 (1994); Carver et al., Biotechnology (NY) 11:1263-1270 (1993); Wright et al., Biotechnology (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., Cell 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, Mol Cell. Biol. 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ulmer et al., Science 259:1745 (1993); introducing nucleic acid constructs into embryonic pleuripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., Cell 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," Intl. Rev. Cytol. 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campell et al., Nature 380:64-66 (1996); Wilmut et al., Nature 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, i.e., mosaic

animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., Proc. Natl. Acad. Sci. USA 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example, the teaching of Gu et al. (Gu et al., Science 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and reverse transcriptase-PCR(RT-PCR).. Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the need for screening of animals by DNA

analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an experimental model of interest.

Transgenic animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying diseases, disorders, and/or conditions associated with aberrant expression, and in screening for compounds effective in ameliorating such diseases, disorders, and/or conditions.

~~Example 31~~Example 35 - **Knock-Out Animals.**

Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (E.g., see Smithies et al., Nature 317:230-234 (1985); Thomas & Capecchi, Cell 51:503-512 (1987); Thompson et al., Cell 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express polypeptides of the invention in vivo. In another embodiment, techniques known in the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (e.g., see Thomas & Capecchi 1987 and Thompson 1989, supra). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site in vivo using appropriate viral vectors that will be apparent to those of skill in the art.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (e.g., knockouts) are administered to a patient in vivo. Such cells may be obtained from the patient (i.e., animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, blood cells (e.g., lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered in vitro using

recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the patient systemically, e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson, U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying diseases, disorders, and/or conditions associated with aberrant expression, and in screening for compounds effective in ameliorating such diseases, disorders, and/or conditions.

~~Example 32~~Example 36 - Production Of An Antibody.

a) Hybridoma Technology

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing human phosphatase are administered to an animal to induce the production of sera containing polyclonal

antibodies. In a preferred method, a preparation of human phosphatase protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

Monoclonal antibodies specific for protein human phosphatase are prepared using hybridoma technology. (Kohler et al., Nature 256:495 (1975); Kohler et al., Eur. J. Immunol. 6:511 (1976); Kohler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981)). In general, an animal (preferably a mouse) is immunized with human phosphatase polypeptide or, more preferably, with a secreted human phosphatase polypeptide-expressing cell. Such polypeptide-expressing cells are cultured in any suitable tissue culture medium, preferably in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981)). The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the human phosphatase polypeptide.

Alternatively, additional antibodies capable of binding to human phosphatase polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody that binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the human phosphatase protein-specific antibody can be blocked by human phosphatase. Such antibodies comprise anti-idiotypic antibodies to the human phosphatase protein-specific antibody and are used to immunize an animal to induce formation of further human phosphatase protein-specific antibodies.

For in vivo use of antibodies in humans, an antibody is "humanized". Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal

antibodies described above. Methods for producing chimeric and humanized antibodies are known in the art and are discussed herein. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

b) Isolation Of Antibody Fragments Directed

Against human phosphatase From A Library Of scFvs

Naturally occurring V-genes isolated from human PBLs are constructed into a library of antibody fragments which contain reactivities against human phosphatase to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793 incorporated herein by reference in its entirety).

Rescue of the Library. A library of scFvs is constructed from the RNA of human PBLs as described in PCT publication WO 92/01047. To rescue phage displaying antibody fragments, approximately 109 E. coli harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 μg/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to inoculate 50 ml of 2xTY-AMP-GLU, 2 x 108 TU of delta gene 3 helper (M13 delta gene III, see PCT publication WO 92/01047) are added and the culture incubated at 37°C for 45 minutes without shaking and then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 μg/ml ampicillin and 50 ug/ml kanamycin and grown overnight. Phage are prepared as described in PCT publication WO 92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C without shaking and then for a further hour at 37°C with shaking. Cells are spun down (IEC-Centra 8,400 r.p.m. for 10 min), resuspended in 300 ml 2xTY broth containing 100 μg ampicillin/ml and 25 μg kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and concentrated from the culture medium by two PEG-precipitations (Sambrook et al., 1990), resuspended in 2 ml PBS and passed

through a 0.45 μm filter (Minisart NML; Sartorius) to give a final concentration of approximately 1013 transducing units/ml (ampicillin-resistant clones).

Panning of the Library. Immunotubes (Nunc) are coated overnight in PBS with 4 ml of either 100 μg/ml or 10 μg/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately 1013 TU of phage is applied to the tube and incubated for 30 minutes at room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml of mid-log E. coli TG1 by incubating eluted phage with bacteria for 30 minutes at 37°C. The E. coli are then plated on TYE plates containing 1% glucose and 100 μg/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection. This process is then repeated for a total of 4 rounds of affinity purification with tube-washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

Characterization of Binders. Eluted phage from the 3rd and 4th rounds of selection are used to infect E. coli HB 2151 and soluble scFv is produced (Marks, et al., 1991) from single colonies for assay. ELISAs are performed with microtitre plates coated with either 10 pg/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see, e.g., PCT publication WO 92/01047) and then by sequencing. These ELISA positive clones may also be further characterized by techniques known in the art, such as, for example, epitope mapping, binding affinity, receptor signal transduction, ability to block or competitively inhibit antibody/antigen binding, and competitive agonistic or antagonistic activity.

~~Example 33~~Example 37 - Assays Detecting Stimulation Or Inhibition Of B Cell Proliferation And Differentiation.

Generation of functional humoral immune responses requires both soluble and cognate signaling between B-lineage cells and their microenvironment. Signals may impart a positive stimulus that allows a B-lineage cell to continue its programmed development, or a negative

stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous stimulatory and inhibitory signals have been found to influence B cell responsiveness including IL-2, IL-4, IL-5, IL-6, IL-7, IL10, IL-13, IL-14 and IL-15. Interestingly, these signals are by themselves weak effectors but can, in combination with various co-stimulatory proteins, induce activation, proliferation, differentiation, homing, tolerance and death among B cell populations.

One of the best studied classes of B-cell co-stimulatory proteins is the TNF-superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays which allow for the detection and/or observation of the proliferation and differentiation of these B-cell populations and their precursors are valuable tools in determining the effects various proteins may have on these B-cell populations in terms of proliferation and differentiation. Listed below are two assays designed to allow for the detection of the differentiation, proliferation, or inhibition of B-cell populations and their precursors.

In Vitro Assay- Purified polypeptides of the invention, or truncated forms thereof, is assessed for its ability to induce activation, proliferation, differentiation or inhibition and/or death in B-cell populations and their precursors. The activity of the polypeptides of the invention on purified human tonsillar B cells, measured qualitatively over the dose range from 0.1 to 10,000 ng/mL, is assessed in a standard B-lymphocyte co-stimulation assay in which purified tonsillar B cells are cultured in the presence of either formalin-fixed Staphylococcus aureus Cowan I (SAC) or immobilized anti-human IgM antibody as the priming agent. Second signals such as IL-2 and IL-15 synergize with SAC and IgM crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation. Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220).

Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added 105 B-cells suspended in culture medium (RPMI 1640 containing 10% FBS, 5 X 10-5M 2ME, 100U/ml penicillin, 10ug/ml streptomycin, and 10-5 dilution of SAC) in a total volume of 150ul. Proliferation or inhibition is quantitated by a 20h pulse (1uCi/well) with 3H-thymidine (6.7 Ci/mM) beginning 72h post factor addition. The positive and negative controls are IL2 and medium respectively.

In Vivo Assay- BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of a polypeptide of the invention, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal spleens and spleens treated with polypeptides of the invention identify the results of the activity of the polypeptides on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from mice treated with polypeptide is used to indicate whether the polypeptide specifically increases the proportion of ThB+, CD45R(B220)dull B cells over that which is observed in control mice.

Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and polypeptide-treated mice.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 34~~Example 38 - T Cell Proliferation Assay.

A CD3-induced proliferation assay is performed on PBMCs and is measured by the uptake of 3H-thymidine. The assay is performed as follows. Ninety-six well plates are coated with 100 (l/well of mAb to CD3 (HIT3a, Pharmingen) or isotype-matched control mAb (B33.1) overnight at 4 degrees C (1 (g/ml in .05M bicarbonate buffer, pH 9.5), then washed three times with PBS. PBMC are isolated by F/H gradient centrifugation from human peripheral blood and added to quadruplicate wells (5 x 104/well) of mAb coated plates in RPMI containing 10% FCS and P/S in the presence of varying concentrations of polypeptides of the invention (total volume 200 ul). Relevant protein buffer and medium alone are controls. After 48 hr. culture at 37 degrees C, plates are spun for 2 min. at 1000 rpm and 100 (l of supernatant is removed and stored –20 degrees C for measurement of IL-2

(or other cytokines) if effect on proliferation is observed. Wells are supplemented with 100 ul of medium containing 0.5 uCi of 3H-thymidine and cultured at 37 degrees C for 18-24 hr. Wells are harvested and incorporation of 3H-thymidine used as a measure of proliferation. Anti-CD3 alone is the positive control for proliferation. IL-2 (100 U/ml) is also used as a control which enhances proliferation. Control antibody which does not induce proliferation of T cells is used as the negative controls for the effects of polypeptides of the invention.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 35~~Example 39 - Effect Of Polypeptides Of The Invention On The Expression Of MHC Class II, Costimulatory And Adhesion Molecules And Cell Differentiation Of Monocytes And Monocyte-Derived Human Dendritic Cells.

Dendritic cells are generated by the expansion of proliferating precursors found in the peripheral blood: adherent PBMC or elutriated monocytic fractions are cultured for 7-10 days with GM-CSF (50 ng/ml) and IL-4 (20 ng/ml). These dendritic cells have the characteristic phenotype of immature cells (expression of CD1, CD80, CD86, CD40 and MHC class II antigens). Treatment with activating factors, such as TNF-(, causes a rapid change in surface phenotype (increased expression of MHC class I and II, costimulatory and adhesion molecules, downregulation of FC(RII, upregulation of CD83). These changes correlate with increased antigen-presenting capacity and with functional maturation of the dendritic cells.

FACS analysis of surface antigens is performed as follows. Cells are treated 1-3 days with increasing concentrations of polypeptides of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Effect on the production of cytokines. Cytokines generated by dendritic cells, in particular IL-12, are important in the initiation of T-cell dependent immune responses. IL-12 strongly influences the development of Th1 helper T-cell immune response, and induces cytotoxic T and NK cell function. An ELISA is used to measure the IL-12 release as follows. Dendritic cells (106/ml) are

treated with increasing concentrations of polypeptides of the invention for 24 hours. LPS (100 ng/ml) is added to the cell culture as positive control. Supernatants from the cell cultures are then collected and analyzed for IL-12 content using commercial ELISA kit(e.g., R & D Systems (Minneapolis, MN)). The standard protocols provided with the kits are used.

Effect on the expression of MHC Class II, costimulatory and adhesion molecules. Three major families of cell surface antigens can be identified on monocytes: adhesion molecules, molecules involved in antigen presentation, and Fc receptor. Modulation of the expression of MHC class II antigens and other costimulatory molecules, such as B7 and ICAM-1, may result in changes in the antigen presenting capacity of monocytes and ability to induce T cell activation. Increase expression of Fc receptors may correlate with improved monocyte cytotoxic activity, cytokine release and phagocytosis.

FACS analysis is used to examine the surface antigens as follows. Monocytes are treated 1-5 days with increasing concentrations of polypeptides of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Monocyte activation and/or increased survival. Assays for molecules that activate (or alternatively, inactivate) monocytes and/or increase monocyte survival (or alternatively, decrease monocyte survival) are known in the art and may routinely be applied to determine whether a molecule of the invention functions as an inhibitor or activator of monocytes. Polypeptides, agonists, or antagonists of the invention can be screened using the three assays described below. For each of these assays, Peripheral blood mononuclear cells (PBMC) are purified from single donor leukopacks (American Red Cross, Baltimore, MD) by centrifugation through a Histopaque gradient (Sigma). Monocytes are isolated from PBMC by counterflow centrifugal elutriation.

Monocyte Survival Assay. Human peripheral blood monocytes progressively lose viability when cultured in absence of serum or other stimuli. Their death results from internally regulated process (apoptosis). Addition to the culture of activating factors, such as TNF-alpha dramatically improves cell survival and prevents DNA fragmentation. Propidium iodide (PI) staining is used to measure apoptosis as follows. Monocytes are cultured for 48 hours in polypropylene tubes in serum-free medium (positive control), in the presence of 100 ng/ml TNF-alpha (negative control), and in

the presence of varying concentrations of the compound to be tested. Cells are suspended at a concentration of 2 x 106/ml in PBS containing PI at a final concentration of 5 (g/ml, and then incubated at room temperature for 5 minutes before FACScan analysis. PI uptake has been demonstrated to correlate with DNA fragmentation in this experimental paradigm.

Effect on cytokine release. An important function of monocytes/macrophages is their regulatory activity on other cellular populations of the immune system through the release of cytokines after stimulation. An ELISA to measure cytokine release is performed as follows. Human monocytes are incubated at a density of 5x105 cells/ml with increasing concentrations of the a polypeptide of the invention and under the same conditions, but in the absence of the polypeptide. For IL-12 production, the cells are primed overnight with IFN (100 U/ml) in presence of a polypeptide of the invention. LPS (10 ng/ml) is then added. Conditioned media are collected after 24h and kept frozen until use. Measurement of TNF-alpha, IL-10, MCP-1 and IL-8 is then performed using a commercially available ELISA kit(e.g., R & D Systems (Minneapolis, MN)) and applying the standard protocols provided with the kit.

Oxidative burst. Purified monocytes are plated in 96-w plate at 2-1x105 cell/well. Increasing concentrations of polypeptides of the invention are added to the wells in a total volume of 0.2 ml culture medium (RPMI 1640 + 10% FCS, glutamine and antibiotics). After 3 days incubation, the plates are centrifuged and the medium is removed from the wells. To the macrophage monolayers, 0.2 ml per well of phenol red solution (140 mM NaCl, 10 mM potassium phosphate buffer pH 7.0, 5.5 mM dextrose, 0.56 mM phenol red and 19 U/ml of HRPO) is added, together with the stimulant (200 nM PMA). The plates are incubated at 37(C for 2 hours and the reaction is stopped by adding 20 µl 1N NaOH per well. The absorbance is read at 610 nm. To calculate the amount of H2O2 produced by the macrophages, a standard curve of a H2O2 solution of known molarity is performed for each experiment.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 36~~Example 40 - Biological Effects of human phosphatase Polypeptides of the Invention.

Astrocyte and Neuronal Assays.

Recombinant polypeptides of the invention, expressed in Escherichia coli and purified as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the proliferation of glial fibrillary acidic protein immunopositive cells, astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate a polypeptide of the invention's activity on these cells.

Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons in vitro have demonstrated increases in both neuron survival and neurite outgrowth (Walicke et al., "Fibroblast growth factor promotes survival of dissociated hippocampal neurons and enhances neurite extension." Proc. Natl. Acad. Sci. USA 83:3012-3016. (1986), assay herein incorporated by reference in its entirety). However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical neuronal culture paradigm, the ability of a polypeptide of the invention to induce neurite outgrowth can be compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

Fibroblast and endothelial cell assays.

Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from Cell Applications (San Diego, CA). For proliferation assays, the human lung fibroblasts and dermal microvascular endothelial cells can be cultured at 5,000 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is added to each well to a final concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a

CytoFluor fluorescence reader. For the PGE2 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or polypeptides of the invention with or without IL-1(for 24 hours. The supernatants are collected and assayed for PGE2 by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without polypeptides of the invention IL-1(for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, Cambridge, MA).

Human lung fibroblasts are cultured with FGF-2 or polypeptides of the invention for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used to compare stimulation with polypeptides of the invention.

Parkinson Models.

The loss of motor function in Parkinson's disease is attributed to a deficiency of striatal dopamine resulting from the degeneration of the nigrostriatal dopaminergic projection neurons. An animal model for Parkinson's that has been extensively characterized involves the systemic administration of 1-methyl-4 phenyl 1,2,3,6-tetrahydropyridine (MPTP). In the CNS, MPTP is taken-up by astrocytes and catabolized by monoamine oxidase B to 1-methyl-4-phenyl pyridine (MPP+) and released. Subsequently, MPP+ is actively accumulated in dopaminergic neurons by the high-affinity reuptake transporter for dopamine. MPP+ is then concentrated in mitochondria by the electrochemical gradient and selectively inhibits nicotidamide adenine disphosphate: ubiquinone oxidoreductionase (complex I), thereby interfering with electron transport and eventually generating oxygen radicals.

It has been demonstrated in tissue culture paradigms that FGF-2 (basic FGF) has trophic activity towards nigral dopaminergic neurons (Ferrari et al., Dev. Biol. 1989). Recently, Dr. Unsicker's group has demonstrated that administering FGF-2 in gel foam implants in the striatum results in the near complete protection of nigral dopaminergic neurons from the toxicity associated with MPTP exposure (Otto and Unsicker, J. Neuroscience, 1990).

Based on the data with FGF-2, polypeptides of the invention can be evaluated to determine whether it has an action similar to that of FGF-2 in enhancing dopaminergic neuronal survival in

vitro and it can also be tested in vivo for protection of dopaminergic neurons in the striatum from the damage associated with MPTP treatment. The potential effect of a polypeptide of the invention is first examined in vitro in a dopaminergic neuronal cell culture paradigm. The cultures are prepared by dissecting the midbrain floor plate from gestation day 14 Wistar rat embryos. The tissue is dissociated with trypsin and seeded at a density of 200,000 cells/cm2 on polyorthinine-laminin coated glass coverslips. The cells are maintained in Dulbecco's Modified Eagle's medium and F12 medium containing hormonal supplements (N1). The cultures are fixed with paraformaldehyde after 8 days in vitro and are processed for tyrosine hydroxylase, a specific marker for dopaminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic rats. The culture medium is changed every third day and the factors are also added at that time.

Since the dopaminergic neurons are isolated from animals at gestation day 14, a developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive neurons would represent an increase in the number of dopaminergic neurons surviving in vitro. Therefore, if a polypeptide of the invention acts to prolong the survival of dopaminergic neurons, it would suggest that the polypeptide may be involved in Parkinson's Disease.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 37~~Example 41 - **The Effect Of The human phosphatase Polypeptides Of The Invention On The Growth Of Vascular Endothelial Cells.**

On day 1, human umbilical vein endothelial cells (HUVEC) are seeded at 2-5x104 cells/35 mm dish density in M199 medium containing 4% fetal bovine serum (FBS), 16 units/ml heparin, and 50 units/ml endothelial cell growth supplements (ECGS, Biotechnique, Inc.). On day 2, the medium is replaced with M199 containing 10% FBS, 8 units/ml heparin. A polypeptide having the amino acid sequence of SEQ ID NO:150, 152, 8, 10, 42, or 109, and positive controls, such as VEGF and basic FGF (bFGF) are added, at varying concentrations. On days 4 and 6, the medium is replaced. On day 8, cell number is determined with a Coulter Counter.

An increase in the number of HUVEC cells indicates that the polypeptide of the invention may proliferate vascular endothelial cells.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 38~~Example 42 - **Stimulatory Effect Of Polypeptides Of The Invention On The Proliferation Of Vascular Endothelial Cells.**

For evaluation of mitogenic activity of growth factors, the colorimetric MTS (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)2H-tetrazolium) assay with the electron coupling reagent PMS (phenazine methosulfate) was performed (CellTiter 96 AQ, Promega). Cells are seeded in a 96-well plate (5,000 cells/well) in 0.1 mL serum-supplemented medium and are allowed to attach overnight. After serum-starvation for 12 hours in 0.5% FBS, conditions (bFGF, VEGF165 or a polypeptide of the invention in 0.5% FBS) with or without Heparin (8 U/ml) are added to wells for 48 hours. 20 mg of MTS/PMS mixture (1:0.05) are added per well and allowed to incubate for 1 hour at 37°C before measuring the absorbance at 490 nm in an ELISA plate reader. Background absorbance from control wells (some media, no cells) is subtracted, and seven wells are performed in parallel for each condition. See, Leak et al. In Vitro Cell. Dev. Biol. 30A:512-518 (1994).

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 39~~Example 43 - **Inhibition Of PDGF-Induced Vascular Smooth Muscle Cell Proliferation Stimulatory Effect.**

HAoSMC proliferation can be measured, for example, by BrdUrd incorporation. Briefly, subconfluent, quiescent cells grown on the 4-chamber slides are transfected with CRP or FITC-labeled AT2-3LP. Then, the cells are pulsed with 10% calf serum and 6 mg/ml BrdUrd. After 24 h, immunocytochemistry is performed by using BrdUrd Staining Kit (Zymed Laboratories). In brief, the cells are incubated with the biotinylated mouse anti-BrdUrd antibody at 4 degrees C for 2 h after being exposed to denaturing solution and then incubated with the streptavidin-peroxidase and diaminobenzidine. After counterstaining with hematoxylin, the cells are mounted for microscopic examination, and the BrdUrd-positive cells are counted. The BrdUrd index is calculated as a percent

of the BrdUrd-positive cells to the total cell number. In addition, the simultaneous detection of the BrdUrd staining (nucleus) and the FITC uptake (cytoplasm) is performed for individual cells by the concomitant use of bright field illumination and dark field-UV fluorescent illumination. See, Hayashida et al., J. Biol. Chem. 6:271(36):21985-21992 (1996).

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 40~~Example 44 - Stimulation Of Endothelial Migration.

This example will be used to explore the possibility that a polypeptide of the invention may stimulate lymphatic endothelial cell migration.

Endothelial cell migration assays are performed using a 48 well microchemotaxis chamber (Neuroprobe Inc., Cabin John, MD; Falk, W., et al., J. Immunological Methods 1980;33:239-247). Polyvinylpyrrolidone-free polycarbonate filters with a pore size of 8 um (Nucleopore Corp. Cambridge, MA) are coated with 0.1% gelatin for at least 6 hours at room temperature and dried under sterile air. Test substances are diluted to appropriate concentrations in M199 supplemented with 0.25% bovine serum albumin (BSA), and 25 ul of the final dilution is placed in the lower chamber of the modified Boyden apparatus. Subconfluent, early passage (2-6) HUVEC or BMEC cultures are washed and trypsinized for the minimum time required to achieve cell detachment. After placing the filter between lower and upper chamber, 2.5 x 105 cells suspended in 50 ul M199 containing 1% FBS are seeded in the upper compartment. The apparatus is then incubated for 5 hours at 37°C in a humidified chamber with 5% CO2 to allow cell migration. After the incubation period, the filter is removed and the upper side of the filter with the non-migrated cells is scraped with a rubber policeman. The filters are fixed with methanol and stained with a Giemsa solution (Diff-Quick, Baxter, McGraw Park, IL). Migration is quantified by counting cells of three random high-power fields (40x) in each well, and all groups are performed in quadruplicate.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 41~~Example 45 - Stimulation Of Nitric Oxide Production By Endothelial Cells.

Nitric oxide released by the vascular endothelium is believed to be a mediator of vascular endothelium relaxation. Thus, activity of a polypeptide of the invention can be assayed by determining nitric oxide production by endothelial cells in response to the polypeptide.

Nitric oxide is measured in 96-well plates of confluent microvascular endothelial cells after 24 hours starvation and a subsequent 4 hr exposure to various levels of a positive control (such as VEGF-1) and the polypeptide of the invention. Nitric oxide in the medium is determined by use of the Griess reagent to measure total nitrite after reduction of nitric oxide-derived nitrate by nitrate reductase. The effect of the polypeptide of the invention on nitric oxide release is examined on HUVEC.

Briefly, NO release from cultured HUVEC monolayer is measured with a NO-specific polarographic electrode connected to a NO meter (Iso-NO, World Precision Instruments Inc.) (1049). Calibration of the NO elements is performed according to the following equation:

2 KNO2 + 2 KI + 2 H2SO4 6 2 NO + I2 + 2 H2O + 2 K2SO4

The standard calibration curve is obtained by adding graded concentrations of KNO2 (0, 5, 10, 25, 50, 100, 250, and 500 nmol/L) into the calibration solution containing KI and H2SO4. The specificity of the Iso-NO electrode to NO is previously determined by measurement of NO from authentic NO gas (1050). The culture medium is removed and HUVECs are washed twice with Dulbecco's phosphate buffered saline. The cells are then bathed in 5 ml of filtered Krebs-Henseleit solution in 6-well plates, and the cell plates are kept on a slide warmer (Lab Line Instruments Inc.) To maintain the temperature at 37°C. The NO sensor probe is inserted vertically into the wells, keeping the tip of the electrode 2 mm under the surface of the solution, before addition of the different conditions. S-nitroso acetyl penicillamin (SNAP) is used as a positive control. The amount of released NO is expressed as picomoles per 1x106 endothelial cells. All values reported are means of four to six measurements in each group (number of cell culture wells). See, Leak et al. Biochem. and Biophys. Res. Comm. 217:96-105 (1995).

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 42~~Example 46 - **Effect Of human phosphatase Polypepides Of The Invention On Cord Formation In Angiogenesis.**

Another step in angiogenesis is cord formation, marked by differentiation of endothelial cells. This bioassay measures the ability of microvascular endothelial cells to form capillary-like structures (hollow structures) when cultured in vitro.

CADMEC (microvascular endothelial cells) are purchased from Cell Applications, Inc. as proliferating (passage 2) cells and are cultured in Cell Applications' CADMEC Growth Medium and used at passage 5. For the in vitro angiogenesis assay, the wells of a 48-well cell culture plate are coated with Cell Applications' Attachment Factor Medium (200 ml/well) for 30 min. at 37°C. CADMEC are seeded onto the coated wells at 7,500 cells/well and cultured overnight in Growth Medium. The Growth Medium is then replaced with 300 mg Cell Applications' Chord Formation Medium containing control buffer or a polypeptide of the invention (0.1 to 100 ng/ml) and the cells are cultured for an additional 48 hr. The numbers and lengths of the capillary-like chords are quantitated through use of the Boeckeler VIA-170 video image analyzer. All assays are done in triplicate.

Commercial (R&D) VEGF (50 ng/ml) is used as a positive control. b-esteradiol (1 ng/ml) is used as a negative control. The appropriate buffer (without protein) is also utilized as a control.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 43~~Example 47 - **Angiogenic Effect On Chick Chorioallantoic Membrane.**

Chick chorioallantoic membrane (CAM) is a well-established system to examine angiogenesis. Blood vessel formation on CAM is easily visible and quantifiable. The ability of polypeptides of the invention to stimulate angiogenesis in CAM can be examined.

Fertilized eggs of the White Leghorn chick (Gallus gallus) and the Japanese qual (Coturnix coturnix) are incubated at 37.8°C and 80% humidity. Differentiated CAM of 16-day-old chick and 13-day-old qual embryos is studied with the following methods.

On Day 4 of development, a window is made into the egg shell of chick eggs. The embryos are checked for normal development and the eggs sealed with cellotape. They are further incubated until Day 13. Thermanox coverslips (Nunc, Naperville, IL) are cut into disks of about 5 mm in

diameter. Sterile and salt-free growth factors are dissolved in distilled water and about 3.3 mg/ 5 ml are pipetted on the disks. After air-drying, the inverted disks are applied on CAM. After 3 days, the specimens are fixed in 3% glutaraldehyde and 2% formaldehyde and rinsed in 0.12 M sodium cacodylate buffer. They are photographed with a stereo microscope [Wild M8] and embedded for semi- and ultrathin sectioning as described above. Controls are performed with carrier disks alone.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 44~~Example 48 - Angiogenesis Assay Using A Matrigel Implant In Mouse.

In vivo angiogenesis assay of a polypeptide of the invention measures the ability of an existing capillary network to form new vessels in an implanted capsule of murine extracellular matrix material (Matrigel). The protein is mixed with the liquid Matrigel at 4 degree C and the mixture is then injected subcutaneously in mice where it solidifies. After 7 days, the solid "plug" of Matrigel is removed and examined for the presence of new blood vessels. Matrigel is purchased from Becton Dickinson Labware/Collaborative Biomedical Products.

When thawed at 4 degree C the Matrigel material is a liquid. The Matrigel is mixed with a polypeptide of the invention at 150 ng/ml at 4 degrees C and drawn into cold 3 ml syringes. Female C57Bl/6 mice approximately 8 weeks old are injected with the mixture of Matrigel and experimental protein at 2 sites at the midventral aspect of the abdomen (0.5 ml/site). After 7 days, the mice are sacrificed by cervical dislocation, the Matrigel plugs are removed and cleaned (i.e., all clinging membranes and fibrous tissue is removed). Replicate whole plugs are fixed in neutral buffered 10% formaldehyde, embedded in paraffin and used to produce sections for histological examination after staining with Masson's Trichrome. Cross sections from 3 different regions of each plug are processed. Selected sections are stained for the presence of vWF. The positive control for this assay is bovine basic FGF (150 ng/ml). Matrigel alone is used to determine basal levels of angiogenesis.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 45~~Example 49 - Rescue Of Ischemia In Rabbit Lower Limb Model.

To study the in vivo effects of polynucleotides and polypeptides of the invention on ischemia, a rabbit hindlimb ischemia model is created by surgical removal of one femoral arteries as described previously (Takeshita et al., Am J. Pathol 147:1649-1660 (1995)). The excision of the femoral artery results in retrograde propagation of thrombus and occlusion of the external iliac artery. Consequently, blood flow to the ischemic limb is dependent upon collateral vessels originating from the internal iliac artery (Takeshitaet al. Am J. Pathol 147:1649-1660 (1995)). An interval of 10 days is allowed for post-operative recovery of rabbits and development of endogenous collateral vessels. At 10 day post-operatively (day 0), after performing a baseline angiogram, the internal iliac artery of the ischemic limb is transfected with 500 mg naked expression plasmid containing a polynucleotide of the invention by arterial gene transfer technology using a hydrogel-coated balloon catheter as described (Riessen et al. Hum Gene Ther. 4:749-758 (1993); Leclerc et al. J. Clin. Invest. 90: 936-944 (1992)). When a polypeptide of the invention is used in the treatment, a single bolus of 500 mg polypeptide of the invention or control is delivered into the internal iliac artery of the ischemic limb over a period of 1 min. through an infusion catheter. On day 30, various parameters are measured in these rabbits: (a) BP ratio - The blood pressure ratio of systolic pressure of the ischemic limb to that of normal limb; (b) Blood Flow and Flow Reserve - Resting FL: the blood flow during undilated condition and Max FL: the blood flow during fully dilated condition (also an indirect measure of the blood vessel amount) and Flow Reserve is reflected by the ratio of max FL: resting FL; (c) Angiographic Score - This is measured by the angiogram of collateral vessels. A score is determined by the percentage of circles in an overlaying grid that with crossing opacified arteries divided by the total number m the rabbit thigh; (d) Capillary density - The number of collateral capillaries determined in light microscopic sections taken from hindlimbs.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 46~~Example 50 - Effect Of Polypeptides Of The Invention On Vasodilation.

Since dilation of vascular endothelium is important in reducing blood pressure, the ability of polypeptides of the invention to affect the blood pressure in spontaneously hypertensive rats (SHR)

is examined. Increasing doses (0, 10, 30, 100, 300, and 900 mg/kg) of the polypeptides of the invention are administered to 13-14 week old spontaneously hypertensive rats (SHR). Data are expressed as the mean +/- SEM. Statistical analysis are performed with a paired t-test and statistical significance is defined as $p<0.05$ vs. the response to buffer alone.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 47~~Example 51 - Rat Ischemic Skin Flap Model.

The evaluation parameters include skin blood flow, skin temperature, and factor VIII immunohistochemistry or endothelial alkaline phosphatase reaction. Expression of polypeptides of the invention, during the skin ischemia, is studied using in situ hybridization.

The study in this model is divided into three parts as follows:

a) Ischemic skin

b) Ischemic skin wounds

c) Normal wounds

The experimental protocol includes:

a) Raising a 3x4 cm, single pedicle full-thickness random skin flap (myocutaneous flap over the lower back of the animal).

b) An excisional wounding (4-6 mm in diameter) in the ischemic skin (skin-flap).

c) Topical treatment with a polypeptide of the invention of the excisional wounds (day 0, 1, 2, 3, 4 post-wounding) at the following various dosage ranges: 1mg to 100 mg.

d) Harvesting the wound tissues at day 3, 5, 7, 10, 14 and 21 post-wounding for histological, immunohistochemical, and in situ studies.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 48~~Example 52 - Peripheral Arterial Disease Model.

Angiogenic therapy using a polypeptide of the invention is a novel therapeutic strategy to obtain restoration of blood flow around the ischemia in case of peripheral arterial diseases. The experimental protocol includes:

a) One side of the femoral artery is ligated to create ischemic muscle of

the hindlimb, the other side of hindlimb serves as a control.

b) a polypeptide of the invention, in a dosage range of 20 mg - 500 mg, is delivered intravenously and/or intramuscularly 3 times (perhaps more) per week for 2-3 weeks.

c) The ischemic muscle tissue is collected after ligation of the femoral

artery at 1, 2, and 3 weeks for the analysis of expression of a polypeptide of the invention and histology. Biopsy is also performed on the other side of normal muscle of the contralateral hindlimb.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 49~~Example 53 - Ischemic Myocardial Disease Model.

A polypeptide of the invention is evaluated as a potent mitogen capable of stimulating the development of collateral vessels, and restructuring new vessels after coronary artery occlusion. Alteration of expression of the polypeptide is investigated in situ. The experimental protocol includes:

a) The heart is exposed through a left-side thoracotomy in the rat. Immediately, the left coronary artery is occluded with a thin suture (6-0) and the thorax is closed.

b) a polypeptide of the invention, in a dosage range of 20 mg - 500 mg, is delivered intravenously and/or intramuscularly 3 times (perhaps more) per week for 2-4 weeks.

c) Thirty days after the surgery, the heart is removed and cross-sectioned

for morphometric and in situ analyzes.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 50~~Example 54 - Rat Corneal Wound Healing Model.

This animal model shows the effect of a polypeptide of the invention on neovascularization. The experimental protocol includes:

a) Making a 1-1.5 mm long incision from the center of cornea into the stromal layer.

b) Inserting a spatula below the lip of the incision facing the outer corner of the eye.

c) Making a pocket (its base is 1-1.5 mm form the edge of the eye).

d) Positioning a pellet, containing 50ng- 5ug of a polypeptide of the invention, within the pocket.

e) Treatment with a polypeptide of the invention can also be applied topically to the corneal wounds in a dosage range of 20mg - 500mg (daily treatment for five days).

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 51~~Example 55 - Diabetic Mouse and Glucocorticoid-Impaired Wound Healing Models.

A. Diabetic db+/db+ Mouse Model.

To demonstrate that a polypeptide of the invention accelerates the healing process, the genetically diabetic mouse model of wound healing is used. The full thickness wound healing model in the db+/db+ mouse is a well characterized, clinically relevant and reproducible model of impaired wound healing. Healing of the diabetic wound is dependent on formation of granulation tissue and re-epithelialization rather than contraction (Gartner, M.H. et al., J. Surg. Res. 52:389 (1992); Greenhalgh, D.G. et al., Am. J. Pathol. 136:1235 (1990)).

The diabetic animals have many of the characteristic features observed in Type II diabetes mellitus. Homozygous (db+/db+) mice are obese in comparison to their normal heterozygous (db+/+m) littermates. Mutant diabetic (db+/db+) mice have a single autosomal recessive mutation on chromosome 4 (db+) (Coleman et al. Proc. Natl. Acad. Sci. USA 77:283-293 (1982)). Animals show polyphagia, polydipsia and polyuria. Mutant diabetic mice (db+/db+) have elevated blood glucose, increased or normal insulin levels, and suppressed cell-mediated immunity (Mandel et al., J. Immunol. 120:1375 (1978); Debray-Sachs, M. et al., Clin. Exp. Immunol. 51(1):1-7 (1983); Leiter et al., Am. J. of Pathol. 114:46-55 (1985)). Peripheral neuropathy, myocardial complications, and

microvascular lesions, basement membrane thickening and glomerular filtration abnormalities have been described in these animals (Norido, F. et al., Exp. Neurol. 83(2):221-232 (1984); Robertson et al., Diabetes 29(1):60-67 (1980); Giacomelli et al., Lab Invest. 40(4):460-473 (1979); Coleman, D.L., Diabetes 31 (Suppl):1-6 (1982)). These homozygous diabetic mice develop hyperglycemia that is resistant to insulin analogous to human type II diabetes (Mandel et al., J. Immunol. 120:1375-1377 (1978)).

The characteristics observed in these animals suggests that healing in this model may be similar to the healing observed in human diabetes (Greenhalgh, et al., Am. J. of Pathol. 136:1235-1246 (1990)).

Genetically diabetic female C57BL/KsJ (db+/db+) mice and their non-diabetic (db+/+m) heterozygous littermates are used in this study (Jackson Laboratories). The animals are purchased at 6 weeks of age and are 8 weeks old at the beginning of the study. Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. The experiments are conducted according to the rules and guidelines of Bristol-Myers Squibb Company's Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

Wounding protocol is performed according to previously reported methods (Tsuboi, R. and Rifkin, D.B., J. Exp. Med. 172:245-251 (1990)). Briefly, on the day of wounding, animals are anesthetized with an intraperitoneal injection of Avertin (0.01 mg/mL), 2,2,2-tribromoethanol and 2-methyl-2-butanol dissolved in deionized water. The dorsal region of the animal is shaved and the skin washed with 70% ethanol solution and iodine. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is then created using a Keyes tissue punch. Immediately following wounding, the surrounding skin is gently stretched to eliminate wound expansion. The wounds are left open for the duration of the experiment. Application of the treatment is given topically for 5 consecutive days commencing on the day of wounding. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of surgery and at two day intervals thereafter. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

A polypeptide of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology and immunohistochemistry. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Three groups of 10 animals each (5 diabetic and 5 non-diabetic controls) are evaluated: 1) Vehicle placebo control, 2) untreated group, and 3) treated group.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total square area of the wound. Contraction is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm2, the corresponding size of the dermal punch. Calculations are made using the following formula:

[Open area on day 8] - [Open area on day 1] / [Open area on day 1]

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using a Reichert-Jung microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds are used to assess whether the healing process and the morphologic appearance of the repaired skin is altered by treatment with a polypeptide of the invention. This assessment included verification of the presence of cell accumulation, inflammatory cells, capillaries, fibroblasts, re-epithelialization and epidermal maturity (Greenhalgh, D.G. et al., Am. J. Pathol. 136:1235 (1990)). A calibrated lens micrometer is used by a blinded observer.

Tissue sections are also stained immunohistochemically with a polyclonal rabbit anti-human keratin antibody using ABC Elite detection system. Human skin is used as a positive tissue control while non-immune IgG is used as a negative control. Keratinocyte growth is determined by evaluating the extent of reepithelialization of the wound using a calibrated lens micrometer.

Proliferating cell nuclear antigen/cyclin (PCNA) in skin specimens is demonstrated by using anti-PCNA antibody (1:50) with an ABC Elite detection system. Human colon cancer can serve as a positive tissue control and human brain tissue can be used as a negative tissue control. Each specimen includes a section with omission of the primary antibody and substitution with non-

immune mouse IgG. Ranking of these sections is based on the extent of proliferation on a scale of 0-8, the lower side of the scale reflecting slight proliferation to the higher side reflecting intense proliferation.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

B. Steroid Impaired Rat Model

The inhibition of wound healing by steroids has been well documented in various in vitro and in vivo systems (Wahl, Glucocorticoids and Wound healing. In: Anti-Inflammatory Steroid Action: Basic and Clinical Aspects. 280-302 (1989); Wahlet al., J. Immunol. 115: 476-481 (1975); Werb et al., J. Exp. Med. 147:1684-1694 (1978)). Glucocorticoids retard wound healing by inhibiting angiogenesis, decreasing vascular permeability (Ebert et al., An. Intern. Med. 37:701-705 (1952)), fibroblast proliferation, and collagen synthesis (Beck et al., Growth Factors. 5: 295-304 (1991); Haynes et al., J. Clin. Invest. 61: 703-797 (1978)) and producing a transient reduction of circulating monocytes (Haynes et al., J. Clin. Invest. 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989)). The systemic administration of steroids to impaired wound healing is a well establish phenomenon in rats (Beck et al., Growth Factors. 5: 295-304 (1991); Haynes et al., J. Clin. Invest. 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989); Pierce et al., Proc. Natl. Acad. Sci. USA 86: 2229-2233 (1989)).

To demonstrate that a polypeptide of the invention can accelerate the healing process, the effects of multiple topical applications of the polypeptide on full thickness excisional skin wounds in rats in which healing has been impaired by the systemic administration of methylprednisolone is assessed.

Young adult male Sprague Dawley rats weighing 250-300 g (Charles River Laboratories) are used in this example. The animals are purchased at 8 weeks of age and are 9 weeks old at the beginning of the study. The healing response of rats is impaired by the systemic administration of methylprednisolone (17mg/kg/rat intramuscularly) at the time of wounding. Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. This study would be conducted according to the rules and guidelines of Bristol-Myers Squibb Corporations Guidelines for the Care and Use of Laboratory Animals.

The wounding protocol is followed according to section A, above. On the day of wounding, animals are anesthetized with an intramuscular injection of ketamine (50 mg/kg) and xylazine (5 mg/kg). The dorsal region of the animal is shaved and the skin washed with 70% ethanol and iodine solutions. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is created using a Keyes tissue punch. The wounds are left open for the duration of the experiment. Applications of the testing materials are given topically once a day for 7 consecutive days commencing on the day of wounding and subsequent to methylprednisolone administration. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of wounding and at the end of treatment. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

The polypeptide of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Four groups of 10 animals each (5 with methylprednisolone and 5 without glucocorticoid) are evaluated: 1) Untreated group 2) Vehicle placebo control 3) treated groups.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total area of the wound. Closure is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm2, the corresponding size of the dermal punch. Calculations are made using the following formula:

[Open area on day 8] - [Open area on day 1] / [Open area on day 1]

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using an Olympus microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic

examination of the wounds allows assessment of whether the healing process and the morphologic appearance of the repaired skin is improved by treatment with a polypeptide of the invention. A calibrated lens micrometer is used by a blinded observer to determine the distance of the wound gap.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 52~~Example 56 - Lymphedema Animal Model.

The purpose of this experimental approach is to create an appropriate and consistent lymphedema model for testing the therapeutic effects of a polypeptide of the invention in lymphangiogenesis and re-establishment of the lymphatic circulatory system in the rat hind limb. Effectiveness is measured by swelling volume of the affected limb, quantification of the amount of lymphatic vasculature, total blood plasma protein, and histopathology. Acute lymphedema is observed for 7-10 days. Perhaps more importantly, the chronic progress of the edema is followed for up to 3-4 weeks.

Prior to beginning surgery, blood sample is drawn for protein concentration analysis. Male rats weighing approximately ~350g are dosed with Pentobarbital. Subsequently, the right legs are shaved from knee to hip. The shaved area is swabbed with gauze soaked in 70% EtOH. Blood is drawn for serum total protein testing. Circumference and volumetric measurements are made prior to injecting dye into paws after marking 2 measurement levels (0.5 cm above heel, at mid-pt of dorsal paw). The intradermal dorsum of both right and left paws are injected with 0.05 ml of 1% Evan's Blue. Circumference and volumetric measurements are then made following injection of dyc into paws.

Using the knee joint as a landmark, a mid-leg inguinal incision is made circumferentially allowing the femoral vessels to be located. Forceps and hemostats are used to dissect and separate the skin flaps. After locating the femoral vessels, the lymphatic vessel that runs along side and underneath the vessel(s) is located. The main lymphatic vessels in this area are then electrically coagulated suture ligated.

Using a microscope, muscles in back of the leg (near the semitendinosis and adductors) are bluntly dissected. The popliteal lymph node is then located. The 2 proximal and 2 distal lymphatic vessels and distal blood supply of the popliteal node are then and ligated by suturing. The popliteal lymph node, and any accompanying adipose tissue, is then removed by cutting connective tissues.

Care is taken to control any mild bleeding resulting from this procedure. After lymphatics are occluded, the skin flaps are sealed by using liquid skin (Vetbond) (AJ Buck). The separated skin edges are sealed to the underlying muscle tissue while leaving a gap of ~0.5 cm around the leg. Skin also may be anchored by suturing to underlying muscle when necessary.

To avoid infection, animals are housed individually with mesh (no bedding). Recovering animals are checked daily through the optimal edematous peak, which typically occurred by day 5-7. The plateau edematous peak are then observed. To evaluate the intensity of the lymphedema, the circumference and volumes of 2 designated places on each paw before operation and daily for 7 days are measured. The effect plasma proteins on lymphedema is determined and whether protein analysis is a useful testing perimeter is also investigated. The weights of both control and edematous limbs are evaluated at 2 places. Analysis is performed in a blind manner.

Circumference Measurements: Under brief gas anesthetic to prevent limb movement, a cloth tape is used to measure limb circumference. Measurements are done at the ankle bone and dorsal paw by 2 different people then those 2 readings are averaged. Readings are taken from both control and edematous limbs.

Volumetric Measurements: On the day of surgery, animals are anesthetized with Pentobarbital and are tested prior to surgery. For daily volumetrics animals are under brief halothane anesthetic (rapid immobilization and quick recovery), both legs are shaved and equally marked using waterproof marker on legs. Legs are first dipped in water, then dipped into instrument to each marked level then measured by Buxco edema software(Chen/Victor). Data is recorded by one person, while the other is dipping the limb to marked area.

Blood-plasma protein measurements: Blood is drawn, spun, and serum separated prior to surgery and then at conclusion for total protein and Ca2+ comparison.

Limb Weight Comparison: After drawing blood, the animal is prepared for tissue collection. The limbs are amputated using a quillitine, then both experimental and control legs are cut at the ligature and weighed. A second weighing is done as the tibio-cacaneal joint is disarticulated and the foot is weighed.

Histological Preparations: The transverse muscle located behind the knee (popliteal) area is dissected and arranged in a metal mold, filled with freezeGel, dipped into cold methylbutane, placed into labeled sample bags at - 80EC until sectioning. Upon sectioning, the muscle is observed under fluorescent microscopy for lymphatics.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 53~~Example 57 - Suppression Of TNF Alpha-Induced Adhesion Molecule Expression By A Polypeptide Of The Invention.

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

Tumor necrosis factor alpha (TNF-a), a potent proinflammatory cytokine, is a stimulator of all three CAMs on endothelial cells and may be involved in a wide variety of inflammatory responses, often resulting in a pathological outcome.

The potential of a polypeptide of the invention to mediate a suppression of TNF-a induced CAM expression can be examined. A modified ELISA assay which uses ECs as a solid phase absorbent is employed to measure the amount of CAM expression on TNF-a treated ECs when co-stimulated with a member of the FGF family of proteins.

To perform the experiment, human umbilical vein endothelial cell (HUVEC) cultures are obtained from pooled cord harvests and maintained in growth medium (EGM-2; Clonetics, San Diego, CA) supplemented with 10% FCS and 1% penicillin/streptomycin in a 37 degree C humidified incubator containing 5% CO2. HUVECs are seeded in 96-well plates at concentrations of 1 x 104 cells/well in EGM medium at 37 degree C for 18-24 hrs or until confluent. The monolayers

are subsequently washed 3 times with a serum-free solution of RPMI-1640 supplemented with 100 U/ml penicillin and 100 mg/ml streptomycin, and treated with a given cytokine and/or growth factor(s) for 24 h at 37 degree C. Following incubation, the cells are then evaluated for CAM expression.

Human Umbilical Vein Endothelial cells (HUVECs) are grown in a standard 96 well plate to confluence. Growth medium is removed from the cells and replaced with 90 ul of 199 Medium (10% FBS). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 ul volumes). Plates are incubated at 37 degree C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100 µl of 0.1% paraformaldehyde-PBS(with Ca++ and Mg++) is added to each well. Plates are held at 4oC for 30 min.

Fixative is then removed from the wells and wells are washed 1X with PBS(+Ca,Mg)+0.5% BSA and drained. Do not allow the wells to dry. Add 10 µl of diluted primary antibody to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10 µg/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37oC for 30 min. in a humidified environment. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA.

Then add 20 µl of diluted ExtrAvidin-Alkaline Phosphatase (1:5,000 dilution) to each well and incubated at 37oC for 30 min. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA. 1 tablet of p-Nitrophenol Phosphate pNPP is dissolved in 5 ml of glycine buffer (pH 10.4). 100 µl of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphatase in glycine buffer: 1:5,000 (100) > 10-0.5 > 10-1 > 10-1.5. 5 µl of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 µl of pNNP reagent must then be added to each of the standard wells. The plate must be incubated at 37oC for 4h. A volume of 50 µl of 3M NaOH is added to all wells. The results are quantified on a plate reader at 405 nm. The background subtraction option is used on blank wells filled with glycine buffer only. The template is set up to indicate the concentration of AP-conjugate in each standard well [5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

~~Example 54~~Example 58 – **Method of Creating N- and C-terminal Deletion Mutants Corresponding to the Human Phosphatase Polypeptides of the Present Invention.**

As described elsewhere herein, the present invention encompasses the creation of N- and C-terminal deletion mutants, in addition to any combination of N- and C-terminal deletions thereof, corresponding to the human phosphatase polypeptides of the present invention. A number of methods are available to one skilled in the art for creating such mutants. Such methods may include a combination of PCR amplification and gene cloning methodology. Although one of skill in the art of molecular biology, through the use of the teachings provided or referenced herein, and/or otherwise known in the art as standard methods, could readily create each deletion mutant of the present invention, exemplary methods are described below using specific BMY_HPP1, BMY_HPP2, BMY_HPP5 and human RET31 deletions as examples.

Briefly, using the isolated cDNA clone encoding the full-length human BMY_HPP1, BMY_HPP2, BMY_HPP5 or RET31 phosphatase polypeptide sequence (as described elsewhere herein, for example), appropriate primers of about 15-25 nucleotides derived from the desired 5' and 3' positions of SEQ ID NO:41, SEQ ID NO:108, SEQ ID NO:149, or SEQ ID NO:151 may be designed to PCR amplify, and subsequently clone, the intended N- and/or C-terminal deletion mutant. Such primers could comprise, for example, an inititation and stop codon for the 5' and 3' primer, respectively. Such primers may also comprise restriction sites to facilitate cloning of the deletion mutant post amplification. Moreover, the primers may comprise additional sequences, such as, for example, flag-tag sequences, kozac sequences, or other sequences discussed and/or referenced herein.

For example, in the case of the N9 to L606 BMY_HPP1 N-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'-GCAGCA GCGGCCGC AATTTCGGATGGAAGGATTATGGTG -3' (SEQ ID NO:167) *NotI*
3' Primer	5'- GCAGCA GTCGAC GAGGCCAGGCTTAGGGCCATC -3' (SEQ ID NO:168) *SalI*

For example, in the case of the M1 to E500 BMY_HPP1 C-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'- GCAGCA GCGGCCGC ATGGAGGCTGGCATTTACTTCTAC -3' (SEQ ID NO:169) *NotI*
3' Primer	5'- GCAGCA GTCGAC CACCCAAGACCACATCAAGCTGC -3' (SEQ ID NO:170) *SalI*

For example, in the case of the L31 to K150 BMY_HPP2 N-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'-GCAGCA GCGGCCGC CTGTTGGACCTGGGCGTGCGGCACC -3' (SEQ ID NO:171) *NotI*
3' Primer	5'- GCAGCA GTCGAC TTTCGTTCGCTGGTAGAACTGGAAG -3' (SEQ ID NO:172) *SalI*

For example, in the case of the M1 to V111 BMY_HPP2 C-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'- GCAGCA GCGGCCGC ATGGGCGTGCAGCCCCCCAACTTC -3' (SEQ ID NO:173) *NotI*
3' Primer	5'- GCAGCA GTCGAC CACCAGGTAACAGGCCAGCATGGTG -3' (SEQ ID NO:174) *SalI*

For example, in the case of the I256 to S665 BMY_HPP5 N-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'-GCAGCA GCGGCCGC ATCGCCTACATCATGAAGAGGATGG -3' (SEQ ID NO:104) *NotI*
3' Primer	5'- GCAGCA GTCGAC GGAGACCTCAATGATTTCCATGCTG -3' (SEQ ID NO:105) *SalI*

For example, in the case of the M1 to Q367 BMY_HPP5 C-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'- GCAGCA GCGGCCGC ATGGCCCATGAGATGATTGGAACTC –3' (SEQ ID NO:106) *NotI*
3' Primer	5'- GCAGCA GTCGAC CTGCACGCTGGGCACGCTGGGCACG -3' (SEQ ID NO:107) *SalI*

For example, in the case of the I157 to S665 RET31 N-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'-GCAGCA GCGGCCGC ATTGGGCCAACCCGAATTCTTCCC –3' (SEQ ID NO:136) *NotI*
3' Primer	5'- GCAGCA GTCGAC GGAGACCTCAATGATTTCCATGCTG –3' (SEQ ID NO:137) *SalI*

For example, in the case of the M1 to K297 RET31 C-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'- GCAGCA GCGGCCGC ATGGCCCATGAGATGATTGGAACTC –3' (SEQ ID NO:138) *NotI*
3' Primer	5'- GCAGCA GTCGAC CTTCTTCTCATAGTCCAGGAGTTGG -3' (SEQ ID NO:139) *SalI*

For example, in the case of the I157 to S660 mRET31 N-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'-GCAGCA GCGGCCGC ATTGGGCCAACTCGAATTCTTCCC –3' (SEQ ID NO:140) *NotI*

3' Primer	5'- GCAGCA GTCGAC AGAGACCTCGATGATCTCCATGCTG -3' (SEQ ID NO:141) *SalI*

For example, in the case of the M1 to T297 mRET31 C-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'- GCAGCA GCGGCCGC ATGGCCCATGAGATGATTGGAACTC -3' (SEQ ID NO:142) *NotI*
3' Primer	5'- GCAGCA GTCGAC CGTCTTCTCATAGTCCATGAGTTGG -3' (SEQ ID NO:143) *SalI*

Representative PCR amplification conditions are provided below, although the skilled artisan would appreciate that other conditions may be required for efficient amplification. A 100 ul PCR reaction mixture may be prepared using 10ng of the template DNA (cDNA clone of Human phosphatase polypeptides), 200 uM 4dNTPs, 1uM primers, 0.25U Taq DNA polymerase (PE), and standard Taq DNA polymerase buffer. Typical PCR cycling condition are as follows:

20-25 cycles:	45 sec, 93 degrees
	2 min, 50 degrees
	2 min, 72 degrees
1 cycle:	10 min, 72 degrees

After the final extension step of PCR, 5U Klenow Fragment may be added and incubated for 15 min at 30 degrees.

Upon digestion of the fragment with the NotI and SalI restriction enzymes, the fragment could be cloned into an appropriate expression and/or cloning vector which has been similarly digested (e.g., pSport1, among others). . The skilled artisan would appreciate that other plasmids could be equally substituted, and may be desirable in certain circumstances. The digested fragment

and vector are then ligated using a DNA ligase, and then used to transform competent E.coli cells using methods provided herein and/or otherwise known in the art.

The 5' primer sequence for amplifying any additional N-terminal deletion mutants may be determined by reference to the following formula:

(S+(X * 3)) to ((S+(X * 3))+25), wherein 'S' is equal to the nucleotide position of the initiating start codon of the human BMY_HPP1, BMY_HPP2, BMY_HPP5 or RET31 phosphatase gene (SEQ ID NO:41, SEQ ID NO:149, SEQ ID NO:151, or SEQ ID NO:108, respectively), and 'X' is equal to the most N-terminal amino acid of the intended N-terminal deletion mutant. The first term will provide the start 5' nucleotide position of the 5' primer, while the second term will provide the end 3' nucleotide position of the 5' primer corresponding to sense strand SEQ ID NO:41, SEQ ID NO:149, SEQ ID NO:151, or SEQ ID NO:108, respectively. Once the corresponding nucleotide positions of the primer are determined, the final nucleotide sequence may be created by the addition of applicable restriction site sequences to the 5' end of the sequence, for example. As referenced herein, the addition of other sequences to the 5' primer may be desired in certain circumstances (e.g., kozac sequences, etc.).

The 3' primer sequence for amplifying any additional N-terminal deletion mutants may be determined by reference to the following formula:

(S+(X * 3)) to ((S+(X * 3))-25), wherein 'S' is equal to the nucleotide position of the initiating start codon of the human BMY_HPP1, BMY_HPP2, BMY_HPP5 or RET31 phosphatase genes (SEQ SEQ ID NO:41, SEQ ID NO:149, SEQ ID NO:151, or SEQ ID NO:108, respectively), and 'X' is equal to the most C-terminal amino acid of the intended N-terminal deletion mutant. The first term will provide the start 5' nucleotide position of the 3' primer, while the second term will provide the end 3' nucleotide position of the 3' primer corresponding to the anti-sense strand of SEQ SEQ ID NO:41, SEQ ID NO:149, SEQ ID NO:151, or SEQ ID NO:108, respectively. Once the corresponding nucleotide positions of the primer are determined, the final nucleotide sequence may be created by the addition of applicable restriction site sequences to the 5' end of the sequence, for example. As referenced herein, the addition of other sequences to the 3' primer may be desired in certain circumstances (e.g., stop codon sequences, etc.). The skilled artisan would appreciate that modifications of the above nucleotide positions may be necessary for optimizing PCR amplification.

The same general formulas provided above may be used in identifying the 5' and 3' primer sequences for amplifying any C-terminal deletion mutant of the present invention. Moreover, the

same general formulas provided above may be used in identifying the 5' and 3' primer sequences for amplifying any combination of N-terminal and C-terminal deletion mutant of the present invention. The skilled artisan would appreciate that modifications of the above nucleotide positions may be necessary for optimizing PCR amplification.

As mentioned above, the same methodology described for BMY_HPP1, BMY_HPP2, BMY_HPP5 or RET31 N- and C-terminal deletion mutants could be applied to creating N- and C-terminal deletion mutants corresponding to HPP_BMY1, HPP_BMY2, HPP_BMY3, HPP_BMY4, HPP_BMY5, RET31, and/or mRET31 as would be appreciated by the skilled artisan.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

~~Example 55~~Example 59 – **Method of Mutating The Human Phosphatases Of The Present Invention Using Site Directed/Site-Specific Mutagenesis.**

In vitro site-directed mutagenesis is an invaluable technique for studying protein structure-function relationships and gene expression, for example, as well as for vector modification. Approaches utilizing single stranded DNA (ssDNA) as the template have been reported (e.g., T.A. Kunkel et al., 1985, *Proc. Natl. Acad. Sci. USA*), 82:488-492; M.A. Vandeyar et al., 1988, *Gene*, 65(1):129-133; M. Sugimoto et al., 1989, *Anal. Biochem.*, 179(2):309-311; and J.W. Taylor et al., 1985, *Nuc. Acids. Res.*, 13(24):8765-8785).

The use of PCR in site-directed mutagenesis accomplishes strand separation by using a denaturing step to separate the complementary strands and to allow efficient polymerization of the PCR primers. PCR site-directed mutagenesis methods thus permit site specific mutations to be incorporated in virtually any double stranded plasmid, thus eliminating the need for re-subcloning into M13-based bacteriophage vectors or single-stranded rescue. (M.P. Weiner et al., 1995, *Molecular Biology: Current Innovations and Future Trends*, Eds. A.M. Griffin and H.G. Griffin, Horizon Scientific Press, Norfolk, UK; and C. Papworth et al., 1996, *Strategies*, 9(3):3-4).

A protocol for performing site-directed mutagenesis, particularly employing the QuikChange™ site-directed mutagenesis kit (Stratagene, La Jolla, CA; U.S. Patent Nos. 5,789,166 and 5,923,419) is provided for making point mutations, to switch or substitute amino acids, and to

delete or insert single or multiple amino acids in the RATL1d6 amino acid sequence of this invention.

Primer Design

For primer design using this protocol, the mutagenic oligonucleotide primers are designed individually according to the desired mutation. The following considerations should be made for designing mutagenic primers: 1) Both of the mutagenic primers must contain the desired mutation and anneal to the same sequence on opposite strands of the plasmid; 2) Primers should be between 25 and 45 bases in length, and the melting temperature (T_m) of the primers should be greater than, or equal to, 78°C. The following formula is commonly used for estimating the T_m of primers: $T = 81.5 + 0.41$ (%GC) – $675/N$ - %mismatch. For calculating T_m, N is the primer length in bases; and values for %GC and % mismatch are whole numbers. For calculating T_m for primers intended to introduce insertions or deletions, a modified version of the above formula is employed: $T = 81.5 + 0.41$ (%GC) – $675/N$, where N does not include the bases which are being inserted or deleted; 3) The desired mutation (deletion or insertion) should be in the middle of the primer with approximately 10-15 bases of correct sequence on both sides; 4) The primers optimally should have a minimum GC content of 40%, and should terminate in one or more C or G bases; 5) Primers need not be 5'-phosphorylated, but must be purified either by fast polynucleotide liquid chromatography (FPLC) or by polyacrylamide gel electrophoresis (PAGE). Failure to purify the primers results in a significant decrease in mutation efficiency; and 6) It is important that primer concentration is in excess. It is suggested to vary the amount of template while keeping the concentration of the primers constantly in excess (QuikChange™ Site-Directed Mutagenesis Kit, Stratagene, La Jolla, CA).

Protocol for Setting Up the Reactions

Using the above-described primer design, two complimentary oligonucleotides containing the desired mutation, flanked by unmodified nucleic acid sequence, are synthesized. The resulting oligonucleotide primers are purified.

A control reaction is prepared using 5 µl 10x reaction buffer (100mM KCl; 100mM $(NH_4)_2SO_4$; 200mM Tris-HCl, pH 8.8; 20mM $MgSO_4$; 1% Triton® X-100; 1 mg/ml nuclease-free bovine serum albumin, BSA); 2 µl (10ng) of pWhitescript™, 4.5-kb control plasmid (5 ng/µl); 1.25

µl (125 ng) of oligonucleotide control primer #1 (34-mer, 100 ng/µl); 1.25 µl (125 ng) of oligonucleotide control primer #2 (34-mer, 100 ng/µl); 1 µl of dNTP mix; double distilled H_2O; to a final volume of 50 µl. Thereafter, 1 µl of DNA polymerase (*PfuTurbo*® DNA Polymerase, Stratagene), (2.5U/µl) is added. *PfuTurbo*® DNA Polymerase is stated to have 6-fold higher fidelity in DNA synthesis than does *Taq* polymerase. To maximize temperature cycling performance, use of thin-walled test tubes is suggested to ensure optimum contact with the heating blocks of the temperature cycler.

The sample reaction is prepared by combining 5 µl of 10x reaction buffer; x µl (5-50 ng) of dsDNA template; x µl (125 ng) of oligonucleotide primer #1; x µl (5-50 ng) of dsDNA template; x µl (125 ng) of oligonucleotide primer #2; 1 µl of dNTP mix; and ddH_2O to a final volume of 50 µl. Thereafter, 1 µl of DNA polymerase (*PfuTurbo* DNA Polymerase, Stratagene), (2.5U/µl) is added.

It is suggested that if the thermal cycler does not have a hot-top assembly, each reaction should be overlaid with approximately 30 µl of mineral oil.

Cycling the Reactions

Each reaction is cycled using the following cycling parameters:

Segment	Cycles	Temperature	Time
1	1	95°C	30 seconds
2	12-18	95°C	30 seconds
		55°C	1 minute
		68°C	2 minutes/kb of plasmid length

For the control reaction, a 12-minute extension time is used and the reaction is run for 12 cycles. Segment 2 of the above cycling parameters is adjusted in accordance with the type of mutation desired. For example, for point mutations, 12 cycles are used; for single amino acid changes, 16 cycles are used; and for multiple amino acid deletions or insertions, 18 cycles are used. Following the temperature cycling, the reaction is placed on ice for 2 minutes to cool the reaction to ≤37°C.

Digesting the Products and Transforming Competent Cells

One µl of the *Dpn*I restriction enzyme (10U/µl) is added directly (below mineral oil overlay) to each amplification reaction using a small, pointed pipette tip. The reaction mixture is gently and thoroughly mixed by pipetting the solution up and down several times. The reaction mixture is then centrifuged for 1 minute in a microcentrifuge. Immediately thereafter, each reaction is incubated at 37°C for 1 hour to digest the parental (i.e., the non-mutated) supercoiled dsDNA.

Competent cells (i.e., XL1-Blue supercompetent cells, Stratagene) are thawed gently on ice. For each control and sample reaction to be transformed, 50 µl of the supercompetent cells are aliquotted to a prechilled test tube (Falcon 2059 polypropylene). Next, 1 µl of the *Dpn*I-digested DNA is transferred from the control and the sample reactions to separate aliquots of the supercompetent cells. The transformation reactions are gently swirled to mix and incubated for 30 minutes on ice. Thereafter, the transformation reactions are heat-pulsed for 45 seconds at 42°C for 2 minutes.

0.5 ml of NZY+ broth, preheated to 42°C is added to the transformation reactions which are then incubated at 37°C for 1 hour with shaking at 225-250 rpm. An aliquot of each transformation reaction is plated on agar plates containing the appropriate antibiotic for the vector. For the mutagenesis and transformation controls, cells are spread on LB-ampicillin agar plates containing 80 µg/ml of X-gal and 20mM MIPTG. Transformation plates are incubated for >16 hours at 37°C.

~~Example 56~~Example 60 - Complementary Polynucleotides Of The BMY_HPP2 Phosphatase Of The Present Invention.

Antisense molecules or nucleic acid sequences complementary to the BMY_HPP2 protein-encoding sequence, or any part thereof, is used to decrease or to inhibit the expression of naturally occurring BMY_HPP2. Although the use of antisense or complementary oligonucleotides comprising about 15 to 35 base-pairs is described, essentially the same procedure is used with smaller or larger nucleic acid sequence fragments. An oligonucleotide based on the coding sequence of BMY_HPP2 protein, as shown in Figure 21, or as depicted in SEQ ID NO:151, for example, is used to inhibit expression of naturally occurring BMY_HPP2. The complementary oligonucleotide is typically designed from the most unique 5' sequence and is used either to inhibit transcription by preventing promoter binding to the coding sequence, or to inhibit

translation by preventing the ribosome from binding to the BMY_HPP2 protein-encoding transcript. However, other regions may also be targeted.

Using an appropriate portion of the signal and/or 5' sequence of SEQ ID NO:151, an effective antisense oligonucleotide includes any of about 15-35 nucleotides spanning the region which translates into the signal or 5' coding sequence, among other regions, of the polypeptide as shown in Figure 21 (SEQ ID NO:152). Appropriate oligonucleotides are designed using OLIGO 4.06 software and the BMY_HPP2 protein coding sequence (SEQ ID NO:151). Preferred oligonucleotides are dideoxy based and are provided below. The oligonucleotides were synthesized using chemistry essentially as described in U.S. Patent No. 5,849,902; which is hereby incorporated herein by reference in its entirety.

ID#	Sequence
13600	GGAUAUCACUACUGCAUUGCCUGGA (SEQ ID NO:179)
13601	UACAGCAGAUCUGUGCAGGCCAGGU (SEQ ID NO:180)
13602	UGAUCACACAGUAGCGGAAGAUGCU (SEQ ID NO:181)
13603	AGGAGUAGCAGAAUGGUUAGCCUUC (SEQ ID NO:182)
13604	UGAAAGCAGGCGAGAUUCGAUCCGA (SEQ ID NO:183)

The BMY_HPP2 polypeptide has been shown to be involved in the regulation of the mammalian cell cycle. Subjecting cells with an effective amount of a pool of all five of the above antisense oligoncleotides resulted in a significant increase in Cyclin D expression/activity providing convincing evidence that BMY_HPP2 at least regulates the activity and/or expression of Cyclin D either directly, or indirectly. Moreover, the results suggest the physiological role of BMY_HPP2 is the negative regulation of Cyclin D activity and/or expression, either directly or indirectly. The Cyclin D assay used is described below and was based upon the analysis of Cyclin D activity as a downstream marker for proliferative signal transduction events.

Transfection of post-quiescent A549 cells With AntiSense Oligonucleotides.

Materials needed:

- A549 cells maintained in DMEM with high glucose (Gibco-BRL) supplemented with 10% Fetal Bovine Serum, 2mM L-Glutamine, and 1X penicillin/streptomycin.
- Opti-MEM (Gibco-BRL)
- Lipofectamine 2000 (Invitrogen)

- Antisense oligomers (Sequitur)
- Polystyrene tubes.
- Tissue culture treated plates.

Quiescent cells were prepared as follows:

Day 0: 300, 000 A549 cells were seeded in a T75 tissue culture flask in 10 ml of A549 media, and incubated in at 37°C, 5% CO_2 in a humidified incubator for 48 hours.

Day 2: The T75 flasks were rocked to remove any loosely adherent cells, and the A549 growth media removed and replenished with 10 ml of fresh A549 media. The cells were cultured for six days without changing the media to create a quiescent cell population.

Day 8: Quiescent cells were plated in multi-well format and transfected with antisense oligonucleotides.

A549 cells were transfected according to the following:

1. Trypsinize T75 flask containing quiescent population of A549 cells.
2. Count the cells and seed 24-well plates with 60K quiescent A549 cells per well.
3. Allow the cells to adhere to the tissue culture plate (approximately 4 hours).
4. Transfect the cells with antisense and control oligonucleotides according to the following:

   a. A 10X stock of lipofectamine 2000 (10 ug/ml is 10X) was prepared, and diluted lipid was allowed to stand at RT for 15 minutes.
   Stock solution of lipofectamine 2000 was 1 mg/ml.
   10 X solution for transfection was 10 ug/mL.
   To prepare 10X solution, dilute 10 ul of lipofectamine 2000 stock per 1 ml of Opti-MEM (serum free media).

   b. A 10X stock of each oligomer was prepared to be used in the transfection.
   Stock solutions of oligomers were at 100 uM in 20 mM HEPES, pH 7.5.
   10X concentration of oligomer was 0.25 uM.
   To prepare the 10X solutions, dilute 2.5 ul of oligomer per 1 ml of Opti-MEM.

c. Equal volumes of the 10X lipofectamine 2000 stock and the 10X oligomer solutions were mixed well, and incubated for 15 minutes at RT to allow complexation of the oligomer and lipid. The resulting mixture was 5X.
d. After the 15 minute complexation, 4 volumes of full growth media was added to the oligomer/lipid complexes (solution was 1X).
e. The media was aspirated from the cells, and 0.5 ml of the 1X oligomer/lipid complexes added to each well.
f. The cells were incubated for 16-24 hours at 37°C in a humidified CO_2 incubator.
g. Cell pellets were harvested for RNA isolation and TaqMan analysis of downstream marker genes.

TaqMan Reactions

Quantitative RT-PCR analysis was performed on total RNA preps that had been treated with DNaseI or poly A selected RNA. The Dnase treatment may be performed using methods known in the art, though preferably using a Qiagen Rneasy kit to purify the RNA samples, wherein DNAse I treatment is performed on the column.

Briefly, a master mix of reagents was prepared according to the following table:

Dnase I Treatment

Reagent	Per r'xn (in uL)
10x Buffer	2.5
Dnase I (1 unit/ul @1 unit per ug sample)	2
DEPC H_2O	0.5
RNA sample @ 0.1 ug/ul (2-3 ug total)	20
Total	25

Next, 5 ul of master mix was aliquoted per well of a 96-well PCR reaction plate (PE part # N801-0560). RNA samples were adjusted to 0.1 ug/ul with DEPC treated H_2O (if necessary), and 20 ul was added to the aliquoted master mix for a final reaction volume of 25 ul.

The wells were capped using strip well caps (PE part # N801-0935), placed in a plate, and briefly spun in a centrifuge to collect all volume in the bottom of the tubes. Generally, a short spin up to 500rpm in a Sorvall RT is sufficient

The plates were incubated at 37°C for 30 mins. Then, an equal volume of 0.1mM EDTA in 10mM Tris was added to each well, and heat inactivated at 70°C for 5 min. The plates were stored at -80°C upon completion.

RT reaction

A master mix of reagents was prepared according to the following table:

RT reaction

Reagent	RT Per Rx'n (in ul)	No RT Per Rx'n (in ul)
10x RT buffer	5	2.5
$MgCl_2$	11	5.5
DNTP mixture	10	5
Random Hexamers	2.5	1.25
Rnase inhibitors	1.25	0.625
RT enzyme	1.25	-
Total RNA 500ng (100ng no RT)	19.0 max	10.125 max
DEPC H_2O	-	-
Total	50uL	25uL

Samples were adjusted to a concentration so that 500ng of RNA was added to each RT rx'n (100ng for the no RT). A maximum of 19 ul can be added to the RT rx'n mixture (10.125 ul for the no RT.) Any remaining volume up to the maximum values was filled with DEPC treated H_2O, so that the total reaction volume was 50 ul (RT) or 25 ul (no RT).

On a 96-well PCR reaction plate (PE part # N801-0560), 37.5 ul of master mix was aliquoted (22.5 ul of no RT master mix), and the RNA sample added for a total reaction volume of 50ul (25 ul, no RT). Control samples were loaded into two or even three different wells in order to have enough template for generation of a standard curve.

The wells were capped using strip well caps (PE part # N801-0935), placed in a plate, and spin briefly in a centrifuge to collect all volume in the bottom of the tubes. Generally, a short spin up to 500rpm in a Sorvall RT is sufficient.

For the RT-PCR reaction, the following thermal profile was used:

- 25°C for 10 min
- 48°C for 30 min
- 95°C for 5 min
- 4°C hold (for 1 hour)
- Store plate @-20°C or lower upon completion.

TaqMan reaction (Template comes from RT plate.)

A master mix was prepared according to the following table:

TaqMan reaction (per well)

Reagent	Per Rx'n (in ul)
TaqMan Master Mix	4.17
100 uM Probe (SEQ ID NO:186)	.025
100 uM Forward primer (SEQ ID NO:184)	.05
100 uM Reverse primer (SEQ ID NO:185)	.05
Template	-
DEPC H_2O	18.21
Total	22.5

The primers used for the RT-PCR reaction is as follows:

Cyclin D primer and probes:

Forward Primer: ACTACCGCCTCACACGCTTC (SEQ ID NO:184)

Reverse Primer: CTTGACTCCAGCAGGGCTTC (SEQ ID NO:185)

TaqMan Probe: ATCAAGTGTGACCCAGACTGCCTCCG (SEQ ID NO:186)

Using a Gilson P-10 repeat pipetter, 22.5 ul of master mix was aliquouted per well of a 96-well optical plate. Then, using P-10 pipetter, 2.5 ul of sample was added to individual wells. Generally, RT samples are run in triplicate with each primer/probe set used, and no RT samples are run once and only with one primer/probe set, often gapdh (or other internal control).

A standard curve is then constructed and loaded onto the plate. The curve has five points plus one no template control (NTC, =DEPC treated H_2O). The curve was made with a high point of 50 ng of sample (twice the amount of RNA in unknowns), and successive samples of 25, 10, 5, and 1 ng. The curve was made from a control sample(s) (see above).

The wells were capped using optical strip well caps (PE part # N801-0935), placed in a plate, and spun in a centrifuge to collect all volume in the bottom of the tubes. Generally, a short spin up to 500rpm in a Sorvall RT is sufficient.

Plates were loaded onto a PE 5700 sequence detector making sure the plate is aligned properly with the notch in the upper right hand corner. The lid was tightened down and run using the 5700 and 5700 quantitation programes and the SYBR probe using the following thermal profile:

- 50°C for 2 min
- 95°C for 10 min
- and the following for 40 cycles:
  - 95°C for 15 sec
  - 60°C for 1 min
- Change the reaction volume to 25ul.

Once the reaction was complete, a manual threshold of around 0.1 was set to minimize the background signal. Additional information relative to operation of the GeneAmp 5700 machine may be found in reference to the following manuals: "GeneAmp 5700 Sequence Detection System Operator Training CD"; and the "User's Manual for 5700 Sequence Detection System"; available from Perkin-Elmer and hereby incorporated by reference herein in their entirety.

Cyclin D1 is a critical regulator of the process of cell division. It has been identified as an early modulator of the G1 phase of the cell cycle, and cyclin D1 expression increases as cells enter

that phase of the cell cycle. It has long been thought that an ability to pharmacologically block cancerous cells in any part of the cell cycle will have a negative impact on the tumor and be beneficial for managing the disease. Support for this rationale comes from the observation that effective drugs such as Taxol block the cell cycle in G2 phase. Importantly, the rapidly dividing cells found in the cancerous state require abundant levels of cyclin D1 to maintain an accelerated rate of proliferation and proceed to S-phase. Most notably, overexpression of cyclinD1 is a hallmark of several types of human tumors, especially breast tumors (J Mammary Gland Biol Neoplasia 1996 Apr;1(2):153-62). As such, it is thought that drugs that affect cyclin D1, directly or indirectly, would block cancer cells from dividing and have a beneficial effect for patients. Such drug targets could lie within the signal transduction pathway between the oncogene ras and the nucleus, where cell cycle modulators control DNA synthesis (J. Biol Chem 2000, Oct 20;275 (42):32649-57). Even more evidence exists suggesting that the Wnt pathway, mediated by the tumor suppressor betacatenin, regulates the cell cycle via transcriptional control of cyclinD1 (Oncogene 2001 Aug 23;20(37):5093-9: PNAS 2000 Apr11;97(8):4262-6). Thus targets influencing beta catenin/TCF4 function could also affect cyclin D1 transcript levels. As mutations in oncogenes such as ras, and tumor suppressors such as beta catenin are common to may cancers, it is obvious that cyclinD1 levels are indicative of the condition of the cell and its preparedness to proliferate, and affecting cyclinD1 levels and activity could be achieved by numerous mechanisms embodied in multiple pathways .

Antisense inhibition of the HPP_BMY2 phosphatase levels provokes a response in A549 cells that indicates the regulatory pathways controlling cydlinD1 levels are affected. This implicates HPP_BMY2 in pathways important for maintenance of the proliferative state and progression through the cell cycle. As stated above, there are numerous pathways that could have either indirect or direct affects on the transcriptional levels of cyclin D1. Importantly, a major part of the pathways implicated involve the regulation of protein activity through phosphorylation. In as much as HPP_BMY2 is a phosphatase enzyme, it is readily conceivable that dephosphorylation of proteins, the counter activity to the kinases in the signal transduction cascades, contributes to the signals determining cell cycle regulation and proliferation, including regulating cyclin D1 levels. Additionally, the complexity of the interactions between proteins in the pathways described also allow for affects on the pathway eliciting compensatory responses. That is, inhibition of one pathway affecting cyclinD1 activity could provoke a more potent response and signal from another pathway of the same end, resulting in upregulation of cyclin D1. Thus, the effect of inhibition of HPP_BMY2

resulting in slight increases in cyclin D1 levels could indicate that one pathway important to cancer is effected in a way to implicate HPP_BMY2 as a potential target for pharmacologic inhibition for cancer treatment, yet a parallel pathway in the context of the experiment would replace HPP_BMY2 and propagate dysregulation of Cyclin D1.

~~Example 57~~Example 61 – Method of Creating RET31 and Truncated RET31 Fusion Protein Constructs And Methods of Expression and Purification Of The Same.

The GST fusion proteins were designed to contain the full-length RET31 protein sequence (SEQ ID NO:109), as well as a C-terminal deletion mutant of the RET31 protein sequence corresponding to amino acids M1 to T302 of SEQ ID NO:109 which was truncated after the phosphatase homology domain ending at about amino acid residue 297 of SEQ ID NO:109.

In order to generate the RET31 fusion proteins, three PCR primers were designed and received from Life Technologies (Gaithersburg, MD). The oligos were:

Oligo number	Name	Sequence
S5972B08	RET31for	5'-CATATGGGATCCATGGCCCATGAGATTG (SEQ ID NO:187)
S5972B09	RET31rev	5'-GGTACCCTCGAGTCAGGAGACCTCAATGAT (SEQ ID NO:188)
S6311A01	RET31rev2-2	5'-GGTACCCTCGAGTCAAGTCTGGTTCTTAAT (SEQ ID NO:189)

Clones containing the original gene sequence of the full-length RET 31 polynucleotide (SEQ ID NO:108) were used as a template for the subsequent PCR. The clone was linearized using a restriction enzyme prior to PCR. PCR was performed using random hexamers and the Expand High Fidelity PCR System (ROCHE). Amplification was achieved using RET31 forward primer (SEQ ID NO:187) paired with either RET31 Rev (SEQ ID NO:188) or Rev2-2 (SEQ ID NO:189), for the full-length cDNA or truncated cDNA respectively. The thermocycler settings were 94°C for 30 sec, 55°C for 30 sec and 72°C for 60 seconds for 25 cycles. The amplimers were gel purified by the QIAgen Extraction kit (QIAgen, Valencia, CA) and ligated, using T4 DNA ligase, into the pGEX 4T3 Vector (Amersham Pharmacia Biotech) and sequenced using standard methods.

Appropriate clones were chosen based upon the sequencing data, and were used for subsequent steps. Protein expression was induced with 0.1mM IPTG over a 5-hour period. The fusion protein was isolated following the methods outlined in Ausubel, et al., 1992, Short Protocols in Molecular Biology, John Wiley and Sons, Inc., pp.16-28 to 16-31., using GST beads (Pierce) and reduced Glutathione (Sigma). The predicted proteins were approximately 100kD for the full-length protein and 60 kD for the truncated protein. To confirm that GST fusion protein was present, the

proteins, along with appropriate markers, were run on a 4-12% NuPage BIS TRIS Gel with Mops buffer and transferred to a PVD membrane at 4°C. The membrane was blocked with 5% nonfat dry milk in TBS, and probed with a rabbit anti-GST antibody (developed in house). A goat anti-rabbit conjugated to HRP secondary antibody (Biorad) was used and the blot was developed with ECL reagent (Amersham Pharmacia Biotech) – data not shown.

~~Example 57~~Example 62 – Method of Assaying the Phosphatase Activity Of The RET31 Polypeptide.

The phosphatase activity for the full-length RET31 and the M1 to T302 C-terminal RET31 GST fusion proteins were measured by assaying the ability of the proteins to hydrolyze para-nitrophenylphosphate, a compound known to be a substrate for phosphatases, as described in Krejsa, C. et al., J. Biol. Chem.. Vol. 272, p.11541-11549, 1997 (which is hereby incorporated in its entirety herein). The proteins are incubated with para-nitrophenylphosphate in a solution containing 10 mM imidazole, pH 7.0, 1 mM EDTA, 2 mM dithiothreitol, and 5 µg/ml BSA for 2 hours with and without sodium orthovanadate (Fisher) prepared in distilled water. The progress of the phosphatase reaction in a 96-well format was monitored by the OD405 nm on a plate reader (Molecular Devices) at 10-minute intervals in the kinetic mode.

The RET31-GST full length (FL), M1 to T302 C-terminal RET31-GST (trunc), or GST alone were purified and assayed for cleavage of para-nitrophenylphosphate (pNPP). The bars represent the average of triplicate determinations, and the standard deviations are as shown. Each protein preparation was assayed in the absence and presence of 2 mM of the phosphatase inhibitor orthovanadate. The full length and truncated versions clearly demonstrated activity compared to the GST protein as shown in Figure 36. In addition, the full length and truncated protein phosphatase activity was blocked by the phosphatase inhibitor vanadate, as shown.

Of particular significance is the unexpected five fold increase in phosphatase activity of the M1 to T302 C-terminal RET31-GST (trunc) fusion protein relative to the RET31-GST full length (FL) fusion protein.

While the described phosphatase assay elucidated the phosphatase activity of the full-length RET31 (SEQ ID NO:109) and M1 to T302 RET31 C-terminal deletion mutant (amino acids 1 to 302 of SEQ ID NO:109), subsequent sequencing of the RET31-GST full length (FL) and M1 to T302 C-terminal RET31-GST (trunc) fusion protein constructs determined that several amino acid mutations

were unintentionally introduced during their construction. The sequences of the RET31 portions of both fusion proteins are provided below. Since the location of these mutations are not within the conserved phosphatase domain nor near any active site residues, it is not believed they would have any effect on the phosphatase activity of either construct. Rather, the observed phosphatase activity is believed to be representative of the wild type RET31 polypeptide sequence (SEQ ID NO:109) for the RET31-GST full length (FL), while the observed phosphatase activity of the M1 to T302 C-terminal RET31-GST (trunc) fusion protein is believed to be representative of the wild type M1 to T302 C-terminal RET31 C-terminal deletion (amino acids M1 to T302 of SEQ ID NO:109). One skilled in the art of molecular biology could easily correct the mutations of both constructs using known methods in conjunction with the information and teachings described herein. Nonetheless, the polypeptide sequences of the RET31 portion of both fusion proteins are encompassed by the present invention.

In preferred embodiments, the following RET31 polypeptide is encompassed by the present invention:

MAHEIGTQIVTERLVALLESGTEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQQDKVLI
TELIQHSAKHKVDIDCSQKVVVYDQSSQDVASLSSDCFLTVLLGKLEKSFNSVHLLAGGFAE
FSRCFPGLCEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCQRDVLNKELMQQNGIGYVLN
ASNTCPKPDFIPESHFLRVPVNDSFCEKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRSATI
AIAYIMKRMDMSLDEAYRFVKEKRPTISPSFNFLGQLLDYEKKIKNQAGASGPKSKLKLLHL
EKPNEPVPAVSEGGQKSETPLSPPCADSATSEAAGQRPVHPASVPSVPSVQPSLLEDSPLVQA
LSGLHLSADRLEDSNKLKRSFSLDIKSVSYSASMAASLHGFSSSEDALEYYKPSTTLDGTNK
LCQFSPVQELSEQTPETSPDKEEASIPKKLQTARPSDSQSKRLHSVRTSSSGTAQRSLLSPLHR
SGSVEDNYHTSFLFGLSTSQQHLTKSAGLGLKGWHSDILAPQTSTPSLTSSWYFATESSHFYS
ASAIYGGSASYSAYSRSQLPTCGDQVYSVRRRQKPSDRADSRRSWHEESPFEKQFKRRSCQ
MEFGESIMSENRSREELGKVGSQSSFSGSMEIIEVS (SEQ ID NO:190). Polynucleotides encoding this polypeptide are also provided.

In preferred embodiments, the following M1 to T302 RET31 polypeptide is encompassed by the present invention:

MAHEIVGTQIVTERLVALLESGTEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQQDKVLITELIQ HSAKHKVDIDCSQKVVVYDQSSQDVASLSSDCFLTVLLGKLEKSFNSVHLLAGGFAEFSRCFPGLCE GKSTLVPTCISQPCLPVANIGPTRILPNLYLGCQRDVLNKELMQQNGIGYVLNASNTCPKPDFIPESHF LRVPVNDSFCEKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRSATIAIAYIMKRMDMSLDEAYRFV KEKRPTISPSFNFLGQLLDYEKKIKNQT (SEQ ID NO:191). Polynucleotides encoding this polypeptide are also provided.

The present invention encompasses the application of this phosphatase activity assay to the other phosphatases of the present invention.

~~Example 58~~Example 63 – Method Of Assessing The Expression Profile Of The RET31 Phosphatase Polypeptides Of The Present Invention At The Level Of The Protein Using Immunohistochemistry

Peptide Selection and Antibody Production

The sequence for the RET31 polypeptide (SEQ ID NO:109) was analyzed by the algorithm of Hopp and Woods to determine potential peptides for synthesis and antibody production. The peptides were then BLASTed against the SWISS-PROT database to determine the uniqueness of the identified peptide and to help predict the specificity of the resulting antibodies. The following RET31 polypeptide fragments were selected according to the methods above for peptide synthesis: KNQTGASGPKSKKLKLLHLE (SEQ ID NO:192); and CKKLQTARPSDSQSKRLHS (SEQ ID NO:193). Rabbit polyclonal antisera was generated for both synthesized RET31 peptides. In order to allow for peptide conjugation to the carrier protein, a cysteine residue was added to the N-terminus of the SEQ ID NO:193 peptide. The third bleeds were subjected to peptide affinity purification, and the resulting antisera were then used as primary antibodies in immunohistochemistry experiments. The antisera for the SEQ ID NO:192 peptide was labeled RET31 antibody 299, while the antisera for the SEQ ID NO:193 peptide was labeled RET31 antibody 469 antibody.

Antibody Titration Protocol and Positive Control Study Results

Antibody titration experiments were conducted with RET31 antibodies 299 and 469 (both rabbit polyclonals) to establish concentrations that would result in minimal background and maximal detection of signal. Serial dilutions were performed at 1:50. 1:100, 1:250, 1:500, and 1:1000. The serial dilution study demonstrated the highest signal-to-noise ratios at dilutions 1:250 and 1:400, on paraffin-embedded, formalin-fixed tissues for both antibodies. These concentrations were used for

the study. RET31 antibodies 299 and 469 were used as primary antibodies, and the principal detection system consisted of a Vector anti-rabbit secondary (BA-1000; DAKO Corp.), a Vector ABC-AP Kit (AK-5000; DAKO Corp.) with a Vector Red substrate kit (SK-5100; DAKO Corp.), which was used to produce a fuchsia-colored deposit. Tissues were also stained with a positive control antibody (CD31) to ensure that the tissue antigens were preserved and accessible for immunohistochemical analysis. Only tissues that stained positive for CD31 were chosen for the remainder of the study. The negative control consisted of performing the entire immunohistochemistry procedure on adjacent sections in the absence of primary antibody. Slides were imaged using a DVC 1310C digital camera coupled to a Nikon microscope. Images were stored as TIFF files using Adobe PhotoShop.

Immunohistochemistry Procedure

Slides containing paraffin sections (LifeSpan BioSciences, Inc.; Seattle, WA) were deparaffinized through xylene and alcohol, rehydrated, and then subjected to the steam method of target retrieval (#S1700; DAKO Corp.; Carpenteria, CA). Immunohistochemical assay techniques are commonly known in the art and are described briefly herein. Immunocytochemical (ICC) experiments were performed on a DAKO autostainer following the procedures and reagents developed by DAKO. Specifically, the slides were blocked with avidin, rinsed, blocked with biotin, rinsed, protein blocked with DAKO universal protein block, machine blown dry, primary antibody, incubated, and the slides rinsed. Biotinylated secondary antibody was applied using the manufacturer's instructions (1 drop/10 ml, or approximately 0.75 µg/mL), incubated, rinsed slides, and applied Vectastain ABC-AP reagent for 30 minutes. Vector Red was used as substrate and prepared according to the manufacturer's instructions just prior to use.

Immunohistochemistry Results

The immunohistochemistry results were consistent with the Northern Blot and RT-PCR expression profiles described elsewhere herein for the RET31 polypeptide. Specifically, moderate to strong staining was observed in normal respiratory epithelial cell bodies and cilia. Types I and II pneumocytes were also moderately positive, as were neutrophils, mast cells, and macrophages in normal lung. In asthmatic patients, respiratory epithelial cell bodies stained less intensely, but cilia continued to stain strongly. Pneumocytes also stained less intensely than normal tissue.

Inflammatory cell staining did not differ from normal tissue. Bronchial smooth muscle stained faintly in normal and asthmatic lungs. Cytoplasmic, diffuse nucleoplasmic, and nucleolar staining was observed in several cell types, including vascular endothelial and respiratory epithelial cells.

Moderate to strong staining was seen in chondrocytes and rimming osteoblasts in degenerative arthritis. In contrast, osteocytes were negative, as was the osteoid matrix. Hematopoetic tissue showed strongly positive cytoplasm and nucleus in myeloid series cells at all stages of maturation. Megakaryocytic and erythroid cells were negative.

Schwann cells and vascular endothelial cells were moderately to strongly positive in normal colon, in contrast to epithelial cells and ganglion cells, which were negative. Inflammatory cells, such as neutrophils, eosinophils, macrophages, and mast wells were strongly positive. Plasma cells showed blush to faint staining. Lymphocytes in normal colon showed strong punctate nuclear and nucleolar staining. In contrast to normal colon, the colon sections with ulcerative colitis showed less prominent nucleolar staining in lymphocytes. Neuroendocrine cells in the epithelium were faintly positive.

Normal lung showed strong cilial staining in the respiratory epithelial cells, with only blush, diffuse, nuclear staining in the cell body of these cells. Pneumocytes were faintly to moderately positive, as were alveolar macrophages and vascular endothelium. Asthmatic lungs continued to show strong cilial staining, but showed blush positivity in normal lung, and were predominately negative in diseased lung. Pneumocyte staining varied from blush to moderately positive in asthmatic lungs. Pneumocyte staining was unchanged from normal lung. Inflammatory cell staining was similar to normal tissue.

Moderate staining was seen in the stratum granulosum in normal skin, whereas the other layers were negative or showed blush positivity. Melanocytes were moderately to strongly positive, as were hair follicles and eccrine and sebaceous glands. Skin with psoriasis showed strong staining in the stratum granulosum, increased from normal skin. In contrast to normal skin, melanocytes in skin were negative. In the psoriasisform dermatitis sample, the staining pattern was similar to that observed in normal skin.

In synovium, the reactive synoviocytes in one sample of rheumatoid arthritis were faintly to moderately positive, in contrast to normal synoviocytes, which were negative or showed blush staining. In the second sample of rheumatoid arthritis, the difference in synoviocyte staining was smaller than in the first sample.

Interesting observations in this study included the very prominent staining of the nucleolus of lymphocytes and other cell types. In inflammatory bowel disease, the lymphocytes did not show nucleolar staining as prominately as in normal colon. Skin with psorisis had very prominent staining of the stratum granulosum, in comparison to normal skin or to the psoriasiform dermatitis sample.

The present invention encompasses the application of this phosphatase activity assay to the other phosphatases of the present invention.

~~Example 59~~Example 64 – Method Of Assessing The Expression Profile Of The Novel Phosphatases of Polypeptides Of The Present Invention Using Expanded mRNA Tissue and Cell Sources

Total RNA from tissues was isolated using the TriZol protocol (Invitrogen) and quantified by determining its absorbance at 260nM. An assessment of the 18s and 28s ribosomal RNA bands was made by denaturing gel electrophoresis to determine RNA integrity.

The specific sequence to be measured was aligned with related genes found in GenBank to identity regions of significant sequence divergence to maximize primer and probe specificity. Gene-specific primers and probes were designed using the ABI primer express software to amplify small amplicons (150 base pairs or less) to maximize the likelihood that the primers function at 100% efficiency. All primer/probe sequences were searched against Public Genbank databases to ensure target specificity. Primers and probes were obtained from ABI.

For BMY_HPP1, the primer probe sequences were as follows

Forward Primer 5'-TCAGAGAATGGGCCAACAAGA-3' (SEQ ID NO:194)
Reverse Primer 5'-CGAAAACGCTCGAGGAATGA-3' (SEQ ID NO:195)
TaqMan Probe5' –CAGGCCTAGGTTCCTCCTCTCGGAAA-3' (SEQ ID NO:196)

For BMY_HPP2, the primer probe sequences were as follows

Forward Primer 5'-TCAGAGAATGGGCCAACAAGA-3' (SEQ ID NO:197)
Reverse Primer 5'-CGAAAACGCTCGAGGAATGA-3' (SEQ ID NO:198)

TaqMan Probe5' –CAGGCCTAGGTTCCTCCTCTCGGAAA-3' (SEQ ID NO:199)

For BMY_HPP4, the primer probe sequences were as follows

Forward Primer 5'-TCAGAGAATGGGCCAACAAGA-3' (SEQ ID NO:200)
Reverse Primer 5'-CGAAAACGCTCGAGGAATGA-3' (SEQ ID NO:201)
TaqMan Probe5' –CAGGCCTAGGTTCCTCCTCTCGGAAA-3' (SEQ ID NO:202)

For BMY_HPP5 (RET31), the primer probe sequences were as follows

Forward Primer 5'-TCAGAGAATGGGCCAACAAGA-3' (SEQ ID NO:203)
Reverse Primer 5'-CGAAAACGCTCGAGGAATGA-3' (SEQ ID NO:204)
TaqMan Probe5' –CAGGCCTAGGTTCCTCCTCTCGGAAA-3' (SEQ ID NO:205)

The same BMY_HPP5 primer probe sequences hybridize to the RET31 mRNA sequences as well. Therefore, the expression profiling for BMY_HPP5 is also representative of the RET31 expression profile as well.

DNA contamination

To access the level of contaminating genomic DNA in the RNA, the RNA was divided into 2 aliquots and one half was treated with Rnasc-free Dnase (Invitrogen). Samples from both the Dnase-treated and non-treated were then subjected to reverse transcription reactions with (RT+) and without (RT-) the presence of reverse transcriptase. TaqMan assays were carried out with gene-specific primers (see above) and the contribution of genomic DNA to the signal detected was evaluated by comparing the threshold cycles obtained with the RT+/RT- non-Dnase treated RNA to that on the RT+/RT- Dnase treated RNA. The amount of signal contributed by genomic DNA in the Dnased RT- RNA must be less that 10% of that obtained with Dnased RT+ RNA. If not the RNA was not used in actual experiments.

Reverse Transcription reaction and Sequence Detection

100ng of Dnase-treated total RNA was annealed to 2.5 µM of the respective gene-specific reverse primer in the presence of 5.5 mM Magnesium Chloride by heating the sample to 72°C for 2 min and then cooling to 55° C for 30 min. 1.25 U/µl of MuLv reverse transcriptase and 500µM of each dNTP was added to the reaction and the tube was incubated at 37° C for 30 min. The sample was then heated to 90°C for 5 min to denature enzyme.

Quantitative sequence detection was carried out on an ABI PRISM 7700 by adding to the reverse transcribed reaction 2.5µM forward and reverse primers, 500µM of each dNTP, buffer and 5U AmpliTaq Gold™. The PCR reaction was then held at 94°C for 12 min, followed by 40 cycles of 94° C for 15 sec and 60° C for 30 sec.

Data handling

The threshold cycle (Ct) of the lowest expressing tissue (the highest Ct value) was used as the baseline of expression and all other tissues were expressed as the relative abundance to that tissue by calculating the difference in Ct value between the baseline and the other tissues and using it as the exponent in $2^{(\Delta Ct)}$

mRNA levels were assayed in samples from three individual donors for each tissue for each human phosphatase polypeptide. Values presented represent the average abundance of each human phosphatase polypeptide for each tissue divided by the average abundance of said polypeptide in the tissue with the lowest level of expression. For example, the lowest expression level detected for each polypeptide is as follows: BMY_HPP1 = blood mononuclear cells; BMY_HPP2 = umbilical cord; BMY_HPP4 = blood mononuclear cells; and BMY_HPP5 (RET31) = umbilical cord. The expanded expression profile of BMY_HPP1, BMY_HPP2, BMY_HPP4, and BMY_HPP5 (RET31), are provided in Figures 26, 30, 34, and 35 and are described elsewhere herein.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further,

the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.--